SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
I	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	i	\=possible nucleotide insertion)
6675	277	1678	GNWPTERMAFLONPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
}		Ì	LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
1	1		RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
1	1		KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
}	1		GTTATKKIDVYLPLHSSODRLLPMTVVTMASARVQDLIGLICWQ
1		Ì	YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
1	1	[GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
Į.	}	1	KEILLKAVKRIKGSCKVSGSRADGVFEEDSQIDIATVQDMLSSH
ļ			HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
ĺ	1		ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
L	L		KASTKFWIKQXPISIDSDLLCAC\DLAEE
6676	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
		1	LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
1	}		RRSNTAQRLEALRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
]	1		KKSLKEKPPISGKOSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
1			GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
1		i	YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
1	ţ	1	GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
ì			KEILLKAVKRKKGSCKVSGSRADGVFEEDSQIDIATVODMLSSH
ì	1	į	HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
j	1		ADTWRQEQIGCCGAACAALRS+DSHKC+EGISGDKVEIDPVTNQ
			KASTKFWIKQKFISIDSDLLCAC\DLAEE
6677	277	1678	GNWFTERMAFLENPTI ILAHIRQSHVTSDETGMCEMVLIDHDVD
1	1		LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
1			RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
1		l	GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
1		Į.	YTSEGREPKLNONVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
1			GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVENTKVTM
		1	KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
!		1	HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
ļ			ADTWROEOIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNO
{	1		KASTKFWIKQKFISIDSDLLCAC\DLAEE
6678	221	865	GPSNQSSGSLS:1VTGCSSYWS*INDTCTILRVLSSNFGRQ*LR
			PFPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS
[.		1	LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG
ł	1	1	FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN
		1 .	HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP
6679	2	786	LEFARGAMPFLGODWRSPGONWVKTVDGWKRFLDEKSGSFVSDL
1	1	1	SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*ONONS\DFH
			QEKWIYVHKGSIKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV
1		}	RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR
1	1	ł	ELLÇTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN
j			NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF
6680	1498	2951	PLCTLPLMPSALLGWAGERNEKOWPLA/PGPGTWQTPVGSISEE
			P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP
}]	/NOVSPPOPM*GAEENGDORGGKEEAGEELHRSSSGLTAAPGF?
1		ł	EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS
1	1	Ì	MORSQAGLPGWEAGLVESPTHHIPALRPSGINATGEAFPSTTCS
}]	SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD
}			POSOGRGPTOGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS
1		1	TIPKKGTRGFGEGPGVLOERNRWVVGRAQGFTSADAAGTAPPGV
1	1]	*LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVANGRHPGPQV
		1	AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH*
1		į .	WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR
	1		FOGGGGG
	1	L	1.40000

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NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine,
ļ	corresponding	to first	Labeucine, Mamethionine, NaAsparagine,
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1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acić	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion;
6681	1169	511	INYIYYNOOORAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE
0001	1103	311	KMTVGVLTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL
1			LAQEADELTLRONLNRKSPHA\VVTLINTKGHH*LINARLTRYO
ł			TLLCENPHKTIEVSNT/LNPATLLLVTESPVKHNCLEVLDSVYS
}		•	SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETSPAPVTPR
	ł		S
6682	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
1 0002	1	1.50	VRRRIELIODFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
ĺ	ļ	[YOLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG
į.	1	{	FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEOGRYLN
1		į	PLOTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
	1		D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
1	{	Í	DLRSDKPLLVKDHOYGLPIKSVHFQDSLDLILSADSRIVKMWNK
1	l		NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
1	{	1	GPAPRWCSFLDNLTEELEENPESNE
6683	105	1238	TVLCGAMOVSSLNEVKIYSLSCGKSLPEWLSDRKKRALOKKDVD
ļ			VRRRIELIODFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
1	<u> </u>		YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG
	1]	FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
ł			PLOTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
ļ	}		D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
Ì			DLRSDKPLLVKDHOYGLPIKSVHFQDSLDLILSADSRIVKMWNK
-	ł		NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
1	ļ		GPAPRWCSFLDNLTEELEENPESNE
6684	1.13	527	GLRGGTSRGRAGREPEFAAGVLCVVAGFCOSPCPPGGRGREAPA
İ	ĺ		PP\SGRRHA*RPA*WLGGPGGDSGGREEGGS/GELQRAMESKMG
}	}		ELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEAS
			RNIVQNYR
6685	25E	1473	KLLGDNFEGFCNKFELSDSENGSNS * QSPL\FDRLFDPDPQKVL
}			QGVI DMKNAVIGNNKQKANLIVLGAVPRLLYLLQQETSSTELKT
}			ECAVVLGSLAMGTENNVKSLLDCHIIPALLQGLLSPDLKFIEAC
1	}		LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTQEYICQ
Ì			IFSHCCKGPDHQTILFNHGAVQNIAHLLTSLSYKVRMQALKCFS
	1		VLAFENPQVSMTLVNVLVDGELLPQIFVKMLQRDKPIEMQLTSA
1	}		KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERLLEERVEGA
			ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK RLDHDLKHAHELROAAFKLYASLGANDEDIRKKVSLGEGRPPVL
}	}	1	TASROGVIST
6686	310	927	DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY
10000	1 310	921	QLFKPSLISWLEQEESRTVORGDFQASEWKVQLKTKELALQQDV
	İ		LGEPTSSGIOMIGSHNGGEVSDVKOCGDVSSEHSCLKTHVRTON
l	{		SENTFECYLYGVDFLTLHKKTSTGEORSVFSHVWKKPSSLNPDV
			VCOKNRCTRKKKAF*LQLTLGKSFH*SIHT
6687	18]	915	EAMLEAPYKKEEDEQORKEVKKDYPSNTTSSTSNSGNETSGSST
5557	10,) ,13	IGETSNRSRDRDRYRRNSRSRSPGRQCRHRSRSWDRRHGSESR
1	1		SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR
1	l		IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV
}			PLAIGLTGORLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR
1	1	Ì	LYVGSLHFNITEDMLRGIFEPFGKV
6688	1025	1	AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF
1	1025	•	SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD
1	<u> </u>		LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS
[STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE
}		}	VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC
			TMSELEELFSLPSPAPLLSKLPTSSGSIAICCQDSGPSDTGRLS
1	1		VCQLWLADSDTGKLSDCQEVVTVGDSGGLTCPELSLGRM*MSLL
1	1	!	- of man montained of the state of the man of the man of the man of the state of th

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
No.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	secuence	Sequence	\=possible nucleotide insertion)
	secuence	ļ	SSAVIFGYSSSSDSRLNTVPTVDLLCPFQTKSST
6689		1299	SSSASYATSATSISDTAFSGSLKLKHGLLSALDSSSRTS*STSS
0003	640	1299	AEDSTFRICSPSVSDTSSDSSGSKDNVLILFSKVSI*SCFSLSS
}	,]	
1			FFSDSISFCFSSSSFCKR*FVSSKVSQNALLSSRLSNGPGGSSK CRNSLTAROLAMSL*ATKF*RNACNPNCLSSKKSAL*LSLNORF
-		}	• • • • • • • • • • • • • • • • • • • •
6690	 	442	GGSASRKPGNISFNSQKCSALSYCCNFVIKPREVSVSSENYPAF
6690	3	442	GTRGKMAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGP
1		1	OOVGAGOTFEYLKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQ
1			YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKNL\H
6691	1		GDGLAIWYTKDRMQP
6037	287	1401	LKTETS EEKARRYKDRPSQLNAVFQEQKKMIQAQESITLEDVAV
1	1	1	DFTWEEWQLLGAAQKDLYRDVMLENYSNLVAVGYQASKPDALFK
 	i	†	LEQGEOLWT1EDGIHSGACSDIWKVDHVLERLOSESLVNRRKPC
	Į.	1	HEHDAFENIVHCSKSQFLLGQNHDIFDLRGKSLKSNLTLVNQSK GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASOKLISTKSOF
1		ł	1SPKHOKTRKLEKHHVCSECGKAFIKKSWLTDHQVMHTGEKPHR
		}	CSLCEKAFSRKFMLTEHQRTHTGEKPYECPECGKAFLKKSRLNI
1			HOKTHTGEKPYICSECGKGFIOKGNLIVHORIHTGEKPYICNEC
1	(/GKGF1CKTCLIAHORFHTER
6692	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
1 0052	1	1 233	ROEGHSOGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
1	1		DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
	Į.		IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
i		1	DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
			SCLVFCPVLWPEYTFWNLFEAILOFOMNHSVLOK
6693	17€	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCOVE
			RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
1		{	DGLMDLARQKFSRLMEEKEKLOKHGVCIRVLGDLHLLPLDLQEL
1	İ	1	IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
1			DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
		l	SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6694	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
1		1	EVHSLGQ1LPQDGLTAEAGPPEAQDPWGSPG1SLPAAH1GFAAA
	1		LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIOLGITHVV
		l	NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6695	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
			EVHSLGOILPODGLTAEAGPPEAODPWGSPGISLPAAHIGFAAA
1		1	LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
	 		NAAAGKFOVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6696	j i	782	PRVRGRVGERWAFLSVPAAMSSEMEPLLLAWSYFRRRKFOLCAD
1			LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMML
			DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL
1	ļ)	RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML
		!	TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD
	 		LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREAEKQIKSS
6697	3	782	PPLFLRRLNSRALRPGSRKVMAVVFASLSGQDVGSFAYLTIKDR
		1	IPQILTKVIDTLHRHKSEFFEKHGEEGVEAEKKAISLLSKLRNE
	i	İ	LOTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYSP
1	})	WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES
}	1	1	IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL
			SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK
6698	666	754	VGSCACAGSCKCKECKCTSCKKSECRAFP
6699	325	492	EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV
			LLGKRKGSVGAGSFQLPGGHLEFGETWEECAORETWEEAALHLK
ı	I	J	NVHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN

CEO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cveteine, D=Aspartic Acid, E=
NC:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
I NC.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=beucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	seguence	\=possible nucleotide insertion)
<u> </u>	Sequence		ESKRIIYNHAFFFQESKWSGGILQ
6700	1098	1392	TOCWRSSTPGMRTHFRTOP/RLECGOGFSOOENGHCMDTNECIO
0,00	1030	1332	FPFVCPRDKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT
			LLLGLCNLLGK
6701	2	1485	AAAGPRTRVRRAAAFEGOPSPSPGLGPTSDKAAAPRTPKRRRLW
9,01		1403	RORO/HPAMLCYVTRPDAVLMEVEVEAKANGEDCLNOVCRRLGI
ļ		1	IEVDYFGLOFTGSKGESLWLNLRNRISQOMDGLAPYRLKLRVKF
			FVEPHLILOEOTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA
Ì		1	OTKFGDYNONTAKYNYEELCAKELSSATLNSIVAKHKELEGTSQ
•			ASAEYOVLOIVSAMENYGIEWHSVRDSEGOKLLIGVGFEGISIC
]			•
\		}	KDDFSPINRIAYPVVOMATQSGKNVYLTVTKESGNSIVLLFKMI STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHLASLF
į .		1	
1	1	1	LNENINLGKKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRNNQ SPSHSPLKSSESSMNCSSCEGLSCOOTRVLOEKLRKLKEAMLCM
l	!		VCCEEEINSTFCPCGHTVCCESCAAQLQVGESAAHFCLQPHLSL
}		1	LLTGSRSQVLAR
6702	397	1971	PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK
1 6702	391	13/1	RAEALLCSRKATVVRDLVAVRMAEEQEFTOLCKLPAQPSHPHCV
İ	i		NNTYRSAOHSOALLRGLIALRDSGILFDVVLVVEGRHIEAHRIL
		1	LAASCDYFKGMFAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS
			ELELSLSNVOETLVAACOLOIPEIIHFCCDFLMSWVDEENILDV
1	1		YRLAELFDLSRLTEOLDTYILKNFVAFSRTDKYROLPLEKVYSL
į	!		LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET
ł			VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ
{		\$	SPOTELRSDFQCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH
			FTASLAPRMSNQGIAVLNNFVYLIGGDNNVQGFRAESRCWRYDP
!			RHNRWFOIQSLQOEHADLSVCVVGRYIYAVAGRDYHNDLNAVER
Ĭ.			YDPATNSWAYVAPLKREVYAHAGATLEGKMYITCGRKGRIT
6703	45	1244	GVGPRAAAMPLELELCPGRWVGGOHPCFIIAEIGONHQGDLDVA
1 0,03	1		KRMIRMAKECGADCAKFOKSELEFKFNRKALERFYTSKHSWGKT
			YGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAVEFLHE
1			LNVPFFKVGSGDTNNFPYLEKTAK/TRGWHSVLRDVCGVQLNDE
	!		TSSWDVLGRVRTSKEKVLMVLVLDYSGRPMVISSGMQSMDTMKQ
l		l	VYOIVKPLNPNFCFLOCTSAYPLOPEDVNLRVISEYQKLFPDIP
	į		IGYSCHETGIAISVAAVALGAKVLERHITLDKTWKGSDHSASLE
			PGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKV
Ι .			KIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDD
]		Ì	TIMEE
6704	82	1007	TMNTRNRVVNSGLGASPASRPTRDPQDPSGRQGELSPVEDQREG
			LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNEIQRIAEQE
1			LANLEKWKEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK
			YKOKLKREESVRIKKEAEEAELOKMKAIOREKSNKLEEKKRLOE
}		ļ ·	NLRREAFREHQQYKTAEFL/RQTEHRIARQKCLSKCCLWPTILN
1		1	MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKRQQQEQE
1	1		RAKIHOTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW
1			GI
6705	1 2	786	RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT
			SYKRKGGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSPD
	-		LKVIYILVRPKAGOTLOHRVFQILDSKLFEKVIEVRPNVHEKIR
		1	AIYADLNONDFAISKEDMOELLSCTNIIFHCAATVRFDDTLRHA
1		Ì	VOLNVTATROLLLMASOMPKLEAFIHISTAYSNCNLKHIDEVIY
1			The state of the s
	1 226	 	PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
6706	130	531	FTHSSSHSQEMLGKLNMLRNDGHFCDITIRVQDKIFRAHKVVL
1]		AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT
			LSINTENIIDVLAAASYMQMFSVASTCSEFMKSSILWNTPNSQP
t	Į.	Į.	EK

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	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	seguence	\=possible nucleotide insertion)
6707	2233	1343	YWSGIGYELOHFHWRKFHFEKKGPPSTCQBRLYESRSRWPCIS*
6/0/	2233	1343	GMVVVGWTAVNGSW*GGOLRCVCVCTSHSSDSTRSSORASKCHS
	!	1	FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NV
		l	SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNNLLC
	1	1	NRRVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEH
		1	TD*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYA
	<u> </u>	<u> </u>	C*RCHWYFEWLLYNHCGDILVACL*RRQL*SSQ
6708	115	1729	TVGSWSRSGRSPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT
	ĺ		GEIIRVVHPHRPCKLALGSDGVRVTMESALTARDRVGVQDFVLL
	1	1	ENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDIQIYSR
	1	1	OHMERYRGVSFYEEPPHLLAVADTVYRALRTERRDQAVMISVES
	1		GAGKTDATKRLLQLYAETCPAPQRGGAVRDRLLQSNPVLEAFGN
	1	1	AKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSRVVHQ
	1		NHGERNFHIFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAK
	1	[VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNIH
	1	1	FAANEESNAQVTTENQLKYLTRLLSVEGSTLREALTHRKIIAKG
			EELLSPLNLEQAAYARDALAKAVYSRTFTWLVGKINRSLASKDV
		1	ESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFI
			ELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGII\SI
			LDE\ECLRPGE .
6709	3	894	PPHEHLFPSGERGPFSFLVSRRGLGPGKMGKKGKKEKKGRGAEK
			TAAKMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQTVELPCPP
	j		PSPRLNASLSVHPEKDELILFGGEYFNGQKTFLYNELYVYNIRK
	1	†	DTWTKVDIPSPPPRRCAHQAVVVPQGGGQLWVFGGEFASPNGEQ
	1		FYHYKDLWVLHLATKTWEOVKSTGGPSGRSGHRMVAWKRQLILF
	Į.		GGFHESTRDYIYYNDVYAFNLDTFTWSKLSPSGTGPTFRSGCQ\
			1PSLPRAASSVYGGYSKQRVKKDVDKGTRHSDMF
6710	158	980	RHKMTNYRVESSSGRAARKMRLALMGPAFIAAIGYIDPGNFATN
	ł		1QAGASFGYQLLWVVVWANLMAML1QILSAKLGIATGKNLAEQI
		1	RDHYPRPVVWFYWVQAEIIAMATDLAEFIGAAIGFKLILGVSLL
		ł	QGAVLTGIATFLILMLORRGOKPLEKVIGGLLLFVAAAYIVELI
		1	FSQPNLAQLGKGMVIPSLPTSEAVFLAAGVL\GATIMPHVI/YI
	1	{	WHSSLTQHLHGGSRQQRYSATKWDVAIAMTIAGPVNLAIMATAA
			SELNFYGHTGVA .
6711	3	347	VTECKTMTCKMSQLERNI * TMINTLHHYSVKLGHPDTLIHGEFK
			ELVRTDLHNILMKENKNDOAI*HIMEDLDTNAHMOIIFKELIML
			MAMLTWSYHDNMHDADYGPGQOHRPG
6712	118	578	PHGQKRTRYPQVRAPGOOPOAQLAMALCLKQVFAKDKTFRPRKR
			FEPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENIDDWIAVHV
	1	{	VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDERQYRR
			PAKLSAPRYMALLMDWIESLI
6713	2485	3	QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE
		1	PDTREMVRAQNKKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI
		1	QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG
		ļ	ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF
	}	1	AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE
	1		MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL
		1	IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV
	}	1	VFVATKHHAEYLTELLTTORVSCAHIYSALDPTARKINLAKFTL
		1	GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA
		1	RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA
	1		GVDGMLGRVPOSVVDEEDSGLOSTLEASLELRGLARVADNAQQQ
			YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL
	1	1	VDSIKNYRSRATIFEINASSRDLCSOVMRAKROKDRKAIARFQO
	ļ]	
		}	GQQGRQEQQGEPVGPAPSRPALQEKQPEKEEBEAGESVEDIFS EVVGRKRQRSGPNRGAKRRREEARQRDQEFYIPYRPKDFDSERG

Depinning Depi	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No. nucleotide location corresponding to first windo acid residue of amino acid residue of amino acid sequence	_	l.	i	
Cocresponding to first anino acid amino acid acid acid acid acid acid acid	1	1 2		
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence Seserine, T-Threonine, V-Valine, amino acid sequence Seserine, T-Threonine, V-Valine, Seserine, T-Threonine, V-Valine, M-Typtophen, Y-Typtophen, Y-	1	,		
to first amino acid residue of amino acid aresidue of amino acid sequence 8-Proline, Q-Glutamine, R-Arginine, 8-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop Coden, /-possible nucleotide deletion) 1-SisGeGaFTODACANDIMGEROCHNUTGEROCHNUTGEROCHNOPERKER FVGGGGERKKIKTEGRYISSSYKBULYGWKKGKGKID-S*-1. 6714 165 1416 6714 165 1416 1816 1816 1816 1816 1816 1817 1816 1816 1817 1817 1817 1817 1817 1817 1817 1817 1818 181	ļ	corresponding	,	
amino acid residue of amino acid sequence and sequence se	ł			
residue of amino acid sequence (Codon, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide insertion) LSISGEGGA-FOOAGCAPULDMOBERGONITAGROCOLHADREKKER FVGGSGDEROCAPULDMOBERGONITAGROCOLHADREKKER FVGGSGDEROCAPULDMOBERGONITAGROCOLHADREKKER FVGGSGDEROCAPULDMOBERGONITAGROCOLHADREKKER FVGGSGDEROCAPULDMOBERGONITAGROCOLHADREKKER FVGGSGDEROCAPULTGEROSCOLHADREKKER FVGGSGDEROCAPULTGEROSCOLHADREKER FVGGSGDEROCAPULTGEROSCOLHADREKER FVGGSGDEROCAPULTGEROSCOLHADREKER FVGGSGDEROCAPULTGEROSCOLHADREKER FVGGSGDEROCAPULTGEROSCOLHADREKER FVGGSGDEROCAPULTGEROSCOLHADREKER FVGGSGDEROCAPULTGER FVGGSGDER FVGGSGDEROCAPULTGER FVGGSGDER FVGGGSGDEROCAPULTGER FVGGSGDER FVGGSGDER FVGGSGDEROCAPULTGER FVGGSGDER FVGGGSGDER FVGGGSGDER FVGGGSGDER FVGGGSGDER FVGGGSGDER FVGGGSG	}	amino acid		
amino acid sequence	}	residue of	amino acid	
Sequence N-possible nucleotide insertion	ļ	amino acid	sequence	
FVGGSGOENKKITTESSEYTISSYKRIDJOKNKKOKKOTIS-SA GRRGILTRREPTEVGCARPILAGAGCIPOPIARPEDASSA LELKTYGOILKORRAOKAALSLORWHPOAALCPO NNCOELLPPPAPPAHI PSGGAPAGAPRAGPYGYCVKVELSVS GONLLDRIVTSKOPFCVLFTENNGKHIETORITETAINNINPAR SKKPVLDPHFEVOKLFRAJEFODKSSKRIDERDFLOOFSCSIK TIVSSKRITFPLILLINDKPARGEITITIAGOELSDRIVITISLAG RRLDKKDLFCKSDPFLEFYKPODDGKMPLUAVERTEVIKYTLDPVW KPPTVPLVSLCIGDEMENPTOWCHVDENGENPTIAGOELSDRIVITISLAG RRLDKKDLFCKSDPFLEFYKPODDGKMPLUAVERTEVIKYTLDPVW KPPTVLVSLCIGDEMENPTOWCHVDENGENPTINPGTYPSY FLDVILIGGCQLMFVGJORKHVDIVASKGIILJSCKINRYN SAINAVGGIIODYDDKMPPALGEGAQLPPDMVSHEFAINPN TWPPCGGVGLIAAAVSACLP 6715 32 493 GPAGAESGSLHCLPATVOALAGAAHSPHGGOPPRRGPLIGGGM CKRCHLGPWGAMFULAVSDGELSSTTGPQQGGGGGSISSISISIS PSGSSPPPTEEDVASWALSSERLLQDPUGLAYFTEFLKKEFS ARMVTENKACKFRQJIPASDT 6716 1 176 GAGGPAPRSFGSEEPFRALERBRNSARAAAKSTAMEETAIWED HTVPLIRVSLCCSK CKRCHLGPWGAMFULAVSDGELSSTTGPQQGGGGGGSISISISISIS PSGSSPPPTEEDFURSAKATAAAKSTAMEETAIWED HTVPLIRVSLCCSK TOTAL STANDAVGGOPPRGGOPPRRGPLIGGGM FEDEPPLEFELGIFRONDFYOTSYSIDDOSOOSYDYGGGGGFSKQVAK YDYSQOGRFVPPDMOOPQOPYTGGIYQFPQAYPASPOOPYANA FEDEPPLEFELGIFROPHINGKTALVHLPLAVADASINNETDLAG DWVFCLAFGATLLLAGKIGGGVVGISAIGCLGMRCLLBILMSMT GVSFGCVASSLVGCLLDMILLSSFAVIFSLGCMVGLILTAGIIG WCSFSASKIFISALAMEGOOLLVAYPCALLYGVFALLSVV VIPTEESLIGLIDKVATACO VIPTEESLIGLIDKVATACO VIPTEESLIGLIDKVATACO VIPTEESLIGLIDKVATACO VVKKSSKARTGLAITIRCAATAANKIKIMSDCSSDHGCET DLDSDDDLKERPMFMMDGSAGONGLSKKISKKRVCSSDDSSDI OVKKSSKARTGLAITIRCAATAANKIKIMSDCSSDHGCET DLDSDDDLKERPMFMMDGSAGONGLSKKISKKRVCSSDDSSDI OVKKSSKARTGLAITIRCAATAANKIKIMSDCGNATHIKKIDAFSP PRESEOREEDSCKHKWEMNPISGNINGDFIAMSQCSSDHGCET DLDSDDDLKERPMFMMDGSAGONGLSKKISKRRVCSSDDSDSI OVKKSSKARTGLAITIRCAATAANKIKIMSDCGNATHIKKIDAFSP PRESEOREEDSCKHKWEMPITGNINGDFIAMSQCSSDHGCET DLDSDDDLKERPMFMMDGSAGONGLSKKISKRRVCSSDDSDSI OVKKSSKARTGLAITIRCAATAANKIKIMSDCGNATHAKIKI BEELKVAAAKKKRADCGGSVTATVLLAGCDBSVVASRGGTEGSALHG IEBELKVAAAKKRAVVIGISSVLAARSKEPTGGGTSGCMAP LAWSYSNOLMKGLGGCKLITYTLLAGCDBSVVASRGGTEGSALHG IEBELKVAAAKKRAVIVIGISVLAGEPGGGVVASGGGTGGRMAP LAWSYSNOLMKGGSFYVAONAGAGGTEGNAP LAWSYSNOLMAGGGGVAVVWORKSSFYB	}	sequence	j -	
GRRGILITRREPRITE/SCEAPPLAQAGC/TOPPHAPRIPLQARSA LELKTKQOILKORRAPOALSO(ENWPOALDO) 6714 165 1416 NNCOELLPPPPAPARI PSGGAPAGGAPHGPQYCVCKVELSVS GQNLLBRUYTSKED PFCULPTENNSKHIETDRITETAINNLBRYS SKRKVLDYHFEEVGLKFALFROGKSKERLDERPELGOFSCSLA RRLDKKDLFKSDPFCLYFTENNSKHIETDRITETAINNLBRYS SKRKVLDYHFEEVGLKAFALFROGKMILVERTEU KYTLDPUN RPTVPLUSLCESDMEKP 10WCVDVDMDGSHDFTGFFGTSVSCSLA RRLDKKDLFKSDPLEFYKRODGKMLWERTEU KYTLDPUN KPFTVPLUSLCESDMEKP 10WCVDVDMDGSHDFTGFFGTSVSC MCEARDSVPLEFFCTNIPKKORKKNYNSIGI ILISCKINRYS FLDYILGGCOLMFTVG1DFTASNGNPLDPSSLHYINFMGTNEYL SAINANGG110PVDSDKMPPALGFGAQLPPDWKVSHEFAINFNP TMPFCSGVDG1AQAYSACLP 6715 32 493 GRAGESSSLHCLPPATVOALAGAAHSPHGGGPPRRGPLIGSGMP GKPHLGVPHGKMVLAVSDGELSSTTGPCQGGGRGSSSLSIHSL PSGGSSPPPTEEDPVASMALSSERLLQOPLGLAYFTEFLKKEPS ARNNYTHMRCARFROQ1PASDT ARTHMATCHCCSK 6716 1 176 GGGGPAPRSFGSEEPRAALSERHLQOPLGLAYFTEFLKKEPS ARNNYTHMRCARFROQ1PASDT 6717 115 896 LFAMSGFENLNTDFVOTSYSIDDDSOGSYDVGGSGGFYSKOVAG VDYSOGGRIPPENDMOPQOPYTGO1YQPTDAYTPASPOPPYGNN FEDEPPLLEBLGINFDHINGKTLTVLHPLAXAGSGINNETPLAG FNVFCLARGATLLLAGK1GRGYYYG1SAIGCLGMPCILNLBMG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSSFNVIFSLIGGMGSILTAGTIG GVSFGCVASVLGYCLLFMILLSGFRYGGSTSGCMGST GVSFGCVASVLGYCLLFMILLSGGARGFLYGANDFLIG LEKKKALDIKKTTO 10599 10599 105957VFTTILSFRAMPGOQLLVATROCLSFRTGMTTFKFGLIFFKDVFL TRESSPTLAGAATAANKILTAGGDRSVVASKRGGTGSAATA LEKKKALDKKRVATAGT GVSFGCCVASVLGARGAGARTAGAATATAGT UNCHAPPARAGTIVTY GRGTWFGCTAGTGATTAGT UNCHAPPARAGTTVTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT				LSISGEGGAFEQQAAGAVLDLMGDEAQNLTRGRQQLKWDRKKKR
LELKTKQOILKORRRACKAALSLORWINCOAALCPO	1			FVGQSGQEDKKKIKTESGRYISSSYKRDLYQKWKQKQKID*S*L
6714 165 1416 NNCOELLPPPAPMANI PSGGRARAGAPRGROVCKVELEVESVE CONLLINGUTSKSDPFCVLPTENNGRNIEDHDFLOOFSCSLA SKREVLDPHFEWQKLKFALFOODKSMKLBEHDFLOOFSCSLA RENDKKULFGKSDPFLOFVERDDCKMMVLBEHDFLOOFSCSLA RENDKKULFGKSDPFLEFYREDDCKMMVLBEHDFLOOFSCSLA RENDKKULFGKSDPFLEFYREDDCKMMVLBEHDFLOOFSCSLA RENDKKULFGKSDPFLEFYREDDCKMMVLBETEVIKYTLDPUM KPFTVPLVSLCDCDMEKPIQVMCYDYDNDGGHDFLOFSVSO MCEARBSVULF FECINPKKGRKKNINNSGILSKAINRDYS SLANAVOGILODYDESMAFPALGFGGLDPDMKVSHEFAINFNP TWPPCGGUDGI AGAYSACLP GRAGAESGSLHCLPATVOALAGANISPIGGOPPRRGPLIGSGEN GKPKHLGVPMGRWULAVSDGELSSTTGPQGQCGCGRGSSLSIHSI PSGRSSPPFTEEDPVSNALSFERLLDDPLGLAFTFEILKKEPS AENNTTHKACERFQLIPASDT AENTTHACERFQLIPASDT AENTTHACE	Í	l]	GRRRGILTRRRPRTEEVGEARPLAQAGCIPGPHAPRHPLQAESA
GONLLINDUTSKSDPFCVLFTENNORMIEVDRTETAINNLINPAF SKKFVLDYHFEVQKLKFALFDQDKSSMRLDEHDFLOFSCISL TIVSSKKITRPLLLINDKPAGKGLITTAAQBLSDNRVITLSLAG RRLDKKDLFCKSDPFLEFYKFODDCKMMLVHETEVIKYTLDFVM KPFTVPLVSLOEDDMEKPIQHCYTOPTDTAGHSDNRVITLSLAG RRLDKKDLFCKSDPFLEFYKFODDCKMMLVHETEVIKYTLDFVM KPFTVPLVSLOEDDMEKPIQHCYTOPTDTAGHSDPILGEFGTSVSQ MCEARDSVPLEFECINPKKQRKKNIYKNSGIILGRSCKINRDYS FLDVILGGCQUMFTVGLDFTAGKGPLDPSSLHYINPMGTNEYL SAIMAVQOIIQDVDSDKMFPALGFGAQLPPDMKVSHEFAINFNP TMPPCGGVDZI AQAYSACLP SAIMAVQOIIQDVDSDKMFPALGFGAQLPPDMKVSHEFAINFNP TMPPCGGVDZI AQAYSACLP SEGSSPPTEEDQVASVALSFERLLQOPLCLAFTFELKKEFS AENNTTWKACERFQQIPASDT GKPKHLGVPNGNAVALSDEELSSTTGPQQGGEGGSSISHSL PSGPSSPPTEEDQVASVALSFERLLQOPLCLAFTFELKKEFS AENNTTWKACERFQQIPASDT FREDESSELSTATEQQUAGGAGGSSISHSL PSGPSSPPTEEDQVASVALSFERLLQOPLCLAFTFELKKEFS AENNTTWKACERFQQIPASDT FREDESSELSTATURGQUAGGAGGSSISHSL PSGPSSPPTEEDQVASVALSFERLLQOPLCLAFTELKKEFS AENNTTWKACERFQQIPASDT FREDESSELSTATURGQUAGGAGGSSISHSL PSGPSSPPTEEDQVASVALSFERLLQOPLCLAFTELKKEFS AENNTTWKACERFQQIPASDT FREDESSELSTATURGCAGAAAAKSTAMEETAINEQ HTVTLIRVSLCCSK TYDYSOOGRFVPPDMMOPQQPYTGQIYQFQGSGGPYSKQYAG YDYSOOGRFVPPDMMOPQQPYTGQIYQFQAGGGGPYSKQYAG YDYSOOGRFVPPDMMOPQQPYTGQIYQFQAGGGGFYSKQYAG YDYSOOGRFVPPDMMOPQQPYTGQIYQFQAGGGGFYSKQYAG YDYSOOGRFVPPDMMOPQQPYTGQIYQFQAGGWGLIHLMSMT GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGILAHLMSGIA GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGILAHLMSGIA GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGILAHLMSGIA GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGILAHLMSGIA GVSFGCVASVLGYCLPMILLSSFAVIFSLGCMVGILAHLMSGIS GVSFGCVASVLGYCLPMILLSGCAGSTGGKAT LEKKKLDIMKTATQ 1 691 PFFPEEDDREDGKCHKMEMPISGALLAGFDFTAGKMTFFKDVA VIFTESSELLDEVORNLYQDVALENDFTAGATTAFCAATAANKILMSDVEDVSLEWVHT RSKNGRKKPLHALACTTAKKLASDCGGSVIGCEVPSEQVACEKPP DPDSEGSTKVLSOALNGSDSSEDMLNSEHHHHETNIHKIDAPSK RKSSSVTSG 6720 3 822 HEVAEEAGGTVYPORGTMFGTKRFCHVIETPEPGKMELIGVFAAA VPITEKSNELIGCOLDKADADENTVILLQCCDASLFQEGGALSTY VPITEKSNELIGCOLDKADADENTVILLQCCABLFQEEGQALSTY VPITEKSNELIGCDLAAAAANTANITVILLQCCABLFQEEGQALSTY VPITEKSNELIGDDLAAAAANTANITURLLQCCABLFQEEGQALSTY VPITEKSNELIGDDLAAAAANTANITURLLQCCABLFQEEGQALST				LELKTKQQILKQRRRAOKAALSLQRWWPQAALCPQ
SKKFULDYHFEEVÇKLKFALFODDKSSMICHENDROSCSCLG TIVSSKKITENGKOLITIANGLESDNRVITISLAG RELDKKDLFGKSDPFLEFYKPGDDGKMMLVERTEVIKYTLDPVM KPFTVELVSLCDEDMERPIQVMCIPIYDNDGGHDFIGEFGYSG MCEARDSVPLEFECINPKKGKKNYKNSGIII ILBGCKINRDYS SATMAVGGIIODYDEDNKHPFALGFGAQLPPDWIKSHEFAINENP TNPFCSGVDGIAQAYSACLP FLDYILIGGCQLMFTVGIDFTASKGPPLDPSSLHYINMETHEYL SATMAVGGIIODYDEDNKHPFALGFGAQLPPDWIKSHEFAINENP TNPFCSGVDGIAQAYSACLP FORGAESGSLAGLEPATVQALAGAAHSPHGGOPRRGPLIGSGMP CKPKHLGVPNGRMULAVSDGELSSTTGPQGQGEGRGSSLSINSL PSGPSSPPTEEPDQVASKALSPERLLQDPLGLAYFTEFLKKEPS ABNVTPNKACERFQQIPASDT 6716 1 176 GAGGPARBSFGSEEPFGALBERNKBARAAAKSTAMEETAINEQ HTVTLIKRSLCCSK HTVTLIKRSLCCSK FINANGERPCLAYSTEDDOSOQSYDYGGSGGFYSKQYAG YDYSOGGRFVPDPMMPQOPYTGOIYQPTQAYTPASPOPFYCMN FEDEPPLLEELGINFPHIWQKTLTVLHPLKVADGSIMNETDLAG PNVFCLAFGATLLJAGKIQFGVYVGISAIGLGWAILTAGIIG MCSFSASKIFTSLLABEGQQLAVYCLLHPLKUSDGSIMNETDLAG PNVFCLAFGATLLJAGKIQFGVYVGISAIGLGWAILTAGIIG MCSFSASKIFTSLLABEGQULAVYPCLLLYGVYPALISVF 6718 290 599 KQSSTVPGTILPSLKWENSGLCKFPETGKWTFKEGLIFKDVA VIFTESELGLLDPVORNLYQDVMLENFRNLSVGHNEPHINVFL LEKKKLDIMKTATQ GYSGCVASVLGYCLLPWILLSSFAVIFSLGGMVGILTAGIIG MCSFSASKIFTSLAABEGQULAVYPCLLSVEYPHLSUGYPHLSUGY VIFTESELGLLDPVORNLYQDVMLENFRNLSVGYSDSDGSCT DLOSDDXKIF ENNPWKDSSAGONGLSRKISKRVCSSDSDGCT DLOSDDXKIF ENNPWKDSSAGONGLSRKISKRVCSSDSDGCT DLOSDDXKIF ENNPWKDSSAGONGLSRKISKRVCSSDSDGCT DLOSDDXKIF ENNPWKDSSAGONGLSRKISKRVCSSDSDGCT DLOSDDXKIF ENNPWKDSASGONGLSRKISKRVCSSDSDGCT VYTEKSNELTQOLDKADABINIVALLOQCDAETFQCEGALSTY ORLYSESILTHWQVAKCVQUKEPDGGUVLSGGGTSGKNAP LMSVSTNQLMKGLGOKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLASPVAGDCCKNNTAVFLP VLUGFRYNSMARHFFFPRILRSLTVFPSLRAPHYQITSLLFSM TQRLYSESILTHWQVAKCVQUKEPDGGUVLSGGGTSGRMAP LMSVSTNQLMKGLGOKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKRVIVIGISVGLASPVAGDCCKNNTAVFLP VLUGFRYNSMARHFFFPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 396 SSWSKTWQALPANUFILLFLIGTPQAADANOQAIVALGGAVE VLUGFRYNSMARHFFFPRILRSLTVFPSLRAPHYQITSLLFFN SVVTLISG FRESKRIRLIGNYSLWLEGGSKEDAGRYWCAVLGOHENYONK OKGRVVSENIK KOLLQSAHESSFFIILSGLTVPOSTLHISAETIL FORGSVSENIK KOLLQSAHESSFFIILSGLTVPOSTLHISAETIL	6714	169	1416	NNCQELLPPPPAPMAH: PSGGAPAAGAAPMGPQYCVCKVELSVS
TIVSSKKITRPLLLINDRPAGKGLITTAAOGUSDNRVITISLAGE RRLDKKULEGKSDPFLEFYKODDCKAMIJVERTBUIKYTI.DPUW KPFTVPLVSLCDGDMEKPIQNCYDDTNDGGHDFIGEFGTSVSQ MCBARDSVPLEFECINFKQRKKRNYKNSGIIILGRSCKINDYS FLDVILGGCQUMFTVGIDTAGGAGPHGFIGEFGTSVSQ MCBARDSVPLEFECINFKQRKKRNYKNSGIIILGRSCKINDYS FLDVILGGCQUMFTVGIDTAGGAGPHGPDMKVSHEFAINFNP TNPPCSGVDGI AQAYSACLP 6715 32 493 GPAGAESGSLUCJPATVQALAGAAHSPIGGQPPRRGLIGSGMP CKPKHLGVPNGRWIALAVSDEGLSSTTGPGQGGEGGSSIS.INSI, DSGPSSPFPTEODVASWALSFERLLQDPLGLAYFTEFLKKEPS ABNNTWNRCERFQGIPASDT 6716 1 176 GAGGPAPRSFGSEEPFAALBERDKMSARAAAKSTAMEETAIWEG HTVTLIHRVSLCCSK HTVTLIHRVSLCCSK ABNNTWNRCERFQGIPASDT 6717 115 896 LFAMSGFENINTDFYGTSYSIDDOSOGSYDYGGSGGFYSKQYAG YDYSQGGRVPPDMMOPQOPYTGOIYQPTQAYTPASPOPFYGNN FEDEPPLLEEGINFDHINGKT.TTJLHELKUSINNETDLAG PNVFCLAFGATLLAGKIOFGYVYGISAIGCLGMFCLLALMSMT GUSFGCVASVLGYCLLPWILLSSFAVITFSLQGMVGILTAGIIG WCSFSASKITISLAMMEQQULAVAYPCALLSVGTNETDLAG 6718 290 599 KGSSTVYGGTLIPPSLKWHSGLCKFFETGGRMTTRKEGLTFKUGA VIFTEEGISLIDEVORNLYYODWLENFRNILLSVGHHEFFROVA VIFTEEGISLIDEVORNLYYODWLENFRNILLSVGHHEFFROVA VIFTEEGISLIDEVORNLYYODWLENFRNILLSVGHHEFFROVA VIFTEEGISLIDEVORNLYYODWLENFRNILLSVGHHEFFROVAT LEKSKALDIMKTATO 0 LONGON LERNISKEWCSSDSSSSL 0 LONGON LENGON LERNISKEWCSSDSSSSL 0 LEKSKALDIMKTATO 0 LEKSKALDIMKTATO 0 LEKSKALDIMKTATO 0 LEKSKALDIMKTATO 0 LEKSKALDIMKTATO 0 LEKSKALDIMKTATO 0 LEKSKALDIMKTATO 0 LEKSKALDIMKTATO 0 LEKSKALDIMKTATO 0 LEKSKALDIMKTATO 0 LONGON LENGON			GONLLDRDVTSKSDPFCVLFTENNGRWIEYDRTETAINNLNPAF	
RELDKKOLEGKSDEPLEFYKRODDGKWMLVERTEVIKYTLOPUW KPFTVPLVSLCDGDMEKPIQVMCYDYDNDGGHDIGEPGTSVSQ MCEARDSVPLEFECIPKKQRKKNYKNSGIILESCKINKDYS FLDVILIGGCQLMFTVGIDTTASKONPLDPSSLHYINPGTMEYL SAIMAVGGIIODYDSDKMPPALGFGAQLEPDWKVSHEFAINPN TWPFCSGVDGIAQAYSACLP 6715 32 493 GPAGAESGSLHCLPATVGALAGAAHSPHGQDPPRGPLIGSGMP CKPKHLGVPNGRMVLAVSDGELSSTTGPQQQGEGRGSSLSIHSL PSGPSSPFPTEEQDVASWALSFERLQDPILLAYFTEFIKKEPS ARNYTWRKACEFFQOIPASWALSFERLQDPILLAYFTEFIKKEPS 6716 1 176 GAGGPARRSFGSEEPRAALERBKWSARAAAAKSTAMEETAIWEQ HTVTLIRUSSLCSK FANNSGFENLATEPGVTSVSIDDGSQGSVDYGGSGGFYSKUYAG VDYSOQGRFVPPDMMOPQOPYTGQIVQPTOAPTVASPQPFYGNN FEDEPPLLEELGINFDHINQKTLTVLHPLKVADGSIMMETDLAG PMVPCLAFGATLLLAGKIQFGYVYGISAIGGLGMFCLINLMSMT GVSFGCVASVLGYCLLPMILLSSFAVIFGKMTFKEGLIFKDVA VIFTESELGLLDPVQRNLYQDWMLENFRNLLSVGHHPFKHDVFL LEKKKLDINKTATO 6719 1 691 PTRPESODREDGKCHKMFEMPISGNLNCDPIAMSQCSSDHGCT DLDSDDDKIERPNNFMKDSASQDMGLSKRISRKRVCSSDSDSSL QVVKKSSKARTGLRITTARCAATAANKIKHSDDEDVSLENVHT RSKNGRKRPLHLACTTAKKKLSDCEGSVVCEVPSEQYACEGKPP DPDSEGSTRVLSOALNGDSDSEDMLNSEHKHRETNIHKIDAPSK RKSSSVTSSC 6720 3 822 HEVABEAGGTVYPQGGTKPGTKRFQHVIETPEPGKWELTGVAA VPITEKSNPLTQDLDKADAENIVALLGQCDAEIFQEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSPNQLMKGLGQKPLYTLINGGCDAEIFQEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSPNQLMKGLGQKPLYTLILAGGRAVSGEGTEGRAAF LMSVSPNQLMKGLGGKPLYTLILAGGCDAEIFQEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSPNQLMKGLGGKPLYTLILAGGCDAEIFGEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSPNQLMKGLGGKPLYTLILAGGCDAEIFGEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSPNQLMKGLGGKPLYTLILAGGGRAVAGREGTEDSALHG LEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNTTAVFLP VLNGFPPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSAL LEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNTTAVFLP VLNGFPPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSALHG LEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNTTAVFLP VLNGFPPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSALH LEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNTTAVFLP VLNGFPPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSALH LEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNTTAVFLP VLNGFPPVSMARHPFPPPRILRSL	}	1		SKKFVLDYHFEEVQKLKFALFDQDKSSMRLDEHDFLGQFSCSLG
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MCEARDSVPLEFECINPKKQRKKKNYKNSGIILLSSCKINRDYS PLDYILGGCQLMFTVGIDFTANGNPLDPSSLIYINPMGTNEYL SAIMAVGQIIQDYDSUMMFPALGFGAQLPFDMKVSHEPAINFNP TWPFCGSVDGIAQAYSACLP GPAGAESGILCLDATVOALAGAAHSPHGQQPPRKGPLJGSGMP GKPKHLGVPNGRMULAVSDGELSSTTGPGQGGGGGSSSLSIHSL PSGPSSPPTEEQPUANSMLSFEELLQDPLGLAYFTEFLKKEPS ARMVTPMKRCERFQQIPASDT	ļ	}		RRLDKKDLFGKSDPFLEFYKPGDDGKWMLVERTEVIKYTLDPVW
FLDVILGGCQLMFTVG1DFTASMGNPLDPSSLHYINPMGTNEYL SAINAVGQ11QDYDDKMFPALGFGAQLPPDWKVSHEPAINFNP TNPPCSGVDG1AQAYSACLP	1	1		KPFTVPLVSLCDGDMEKPIQVMCYDYDNDGGHDFIGEFQTSVSQ
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YDYSOOGRFVPPDMMOPQQPYTGQ1YQPTQAYPASPQPFYGNN FEDEPPLLEELGINFDHIWQKTTT-LHPLKVADGSIMNETDLAG PMVPCLAPGATLLAGKIQFCYVYG1SAIGCLGMFCLLNLMSMT GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGIILTAGIIG WCSFSASKIFISALAMBGQQLLVAYPCALLYGYFALISVF 6718 290 599 KQSSTVPGTILPSLKWENSGLCKFPFTGGKMTTFKEGLTFKDVA VIFTEEBELGLDPVQRILYQDVMLEWFRNLLSVGHWFFKHDVPL LEKEKKLDIMKTATO DUSDDKIEKPNNFMKDSASQDNGLSRKISRKVCSSDSGSCT DLDSDDKIEKPNNFMKDSASQDNGLSRKISRKVCSSDSDSL OVVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSQVACEGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRTNIHKIDAPSK RKSSSVTSSC 4 4 4 4 4 5720 3 822 HEVABEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLLAGGDRSVVASREGTEDSAHGG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCHNTTAVFLP VLVGFNPVSMARHPFFPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 4 5721 3 822 HEVABEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLLAGGDRSVVASREGTEDSAHG FLEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCNNTTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 1 6721 3 90 RSWSKRVWQALPNAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVCVGRPAPDPGK PGRESSRLRLLGNYSLWLEGSKEEDAGRYWGAVLGGHNYQNW GNFDYSMARHPFPPPRILRSLTVAPPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPNAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVCVGRPAPDPGK PGRESSRLRLLGNYSLWLEGSKEEDAGRYWGAVLGHNYQNW GNFDYSMARHPFPPRILRSLTVAPPSLRAPHYQLTSLLFSM GFGRSVSVENIKQLLOSAHKESSFDIILSGLVPGSTTLHSAEIL GNFGRVSVENIKQLLOSAHKESSFDIILSGLVPGSTTLHSAEIL	L			1
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PMVFCLAFGATLLLAGKIOFGYVYGISAIGCLGMFCLLNLMSMT GVSFGCVASVLGYCLLPMILLSSFAVIFSLGCMVGILTAGIIG WCSFGASKIF1SALAMEGQGLUVAYPCALLYGVFALISVF 6718 290 599 KQSSTVPGTTLPSLKWENSGLCKFPETGSKMTTFKEGLTFKDVA VIFTEEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVPL LEKEKLLDIMKTATO DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDBGCET DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDBGSL QVVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHHACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDESGSTKVLSOALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSVTSSG 4720 3 822 HEVAEEAGGTVYPQRGTWFGTRFGHVIETPEPGKNELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRNAF LMSVSFNQLMKGLGGKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFFPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTWFGTKRFGHVIETPEPGKWELTGYEAA VPITEKSNPLTODLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRNAF LMSVSFNGLMKGLGGKPLYTYLIAGGDRSVVASREGTEDSALHG LEUKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE LMSVSFNGLMKGLGGKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE FERSTRALLGNYSLWLEGSSEEDAGRWCCAUCHNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE FERSTRALLGNYSLWLEGSSEEDAGRWCCAUCHNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE FROMFRYSTERLLGNYSLWLEGSSEEDAGRWCCAUCHNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE FROMFRYSTERLLGNYSLWLEGSSEEDAGRWCCAUCHNNTAVFLP FROMFRYSTERLLGNYSLWLEGSSEEDAGRWCCAUCHNNTAVFLP GNEGRVSVENIKQLLQSAHKESSFDIILLSGLVPGSTTLHSAEIL GNEGRVSVENIKQLLQSAHKESSFDIILLSGLVPGSTTLHSAEIL		Į.		
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GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL		1	}	PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGOHHNYONW
GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	6723	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT
AEIAR ILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL	1	1		
	L			AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL

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SEQ	1	Predicted end	Amino acid segment containing signal peptide
ID	, -	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	1	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	: amino acid	P=Proline, C=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrcsine, X=Unknown, *=Stop
	amino acid		
i	1	sequence	Codon, /=possible nucleotide deletion,
	sequence	·	\=possible nucleotide insertion;
			VEVKELOREPLTPEEVOSVREHLGHESDNL
6724	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT
			GNEGRVSVENIKOLLQSAHKESSFDIILSGLVPGSTTLHSAEIL
		•	AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL
ł	1	;	VEVKELQREPLTPEEVQSVREHLGHESDNL
6725	356	722	RRRTPPVILATMODDLMLALRLQEEWNLQEAERDHAQESLSLVD
0723	336	1	
	i		ASWELVDFTPDLQALFVQFNDQFFWGQLEAVEVKWSVRMTLCAG
L	<u> </u>	<u> </u>	ICSYEGKGGMCSIRLSEPLLKLRPRKDLVEVFFV
6726	98	714	HLQKMERKINRREKEKEYEGKHNSLEDIDQGKNCKSTLMTLNVG
	i	1 .	GYLYITQKÇTLTKYPDTFLEGIVNGKILCPFDADGHYFIDRDGL
1			LFRHVLNFLRNGELLLPEGFRENQLLAGEAEFFQLKGLAEEVKS
			RWEKEQLTPRETTFLEITDNHDRSQGLRIFCNAPDFISKIKSRI
	l .		VLVSKSRLDGFPEEFSISSNIIOFKYFIK
6727		83:	FRGMGDERPHYYGKHGTPOKYDPTFKGPIYNRGCTDIICCVFLL
0,2,		1	LAIVGYVAVGIIAWTHGDPRKVIYPTDSRGEFCGQKGTKNENKP
1		1	YLFYFNIVKCASPLVLLEFOCPTPOICVEKCPDRYLTYLNARSS
			RDFEYYKOFCVPGFKNNKGVAEVLRDGDCPAVLIPSKPLARRCF
}			PAIHAYKGVLMVGNETTYEDGHGSRKNITDLVEGAKKANGVLEA
ļ		1	RQLAMRIFEDYTVSWYWDIISLGIAMAMSLLFIILLRFLAGIMG
			RGMIIMGILVLGY
6728	486	935	FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSSVIQVFQQLGCA
	f	ļ	VIDVDVMARHVVOPGYPAHRRIVEVFGTEVLLENGDINRKVLGD
			LIFNOPDRROLLNAITHPEIRKEMMKETFKYFLREPRTSPRGKK
			HVPSALKEADSLMRRDT
6729	259	1191	VGLTGAOSGRTASMGRDORAVAGPALRRWLLLGTVTVGFLAQSV
0,25	253	1132	LAGVKKFDVPCGGRDCSGGCOCYPEKGGRGOPGPVGPOGYNGPP
l	1	1	GLQGFPGLOGRKGDKGERGAPGVTGPKGDVGARGVSGFPGADGI
1		Ì	PGHPGQGGPRGRPGYDGCNGTQGDSGPQGPPGSEGFTGPPGPQG
1	1		PKGQKGEPYALPKEERDRYRGEPGEPGLVGFQGPPGRPGHVGQM
ĺ			GPVGAPGRPGPPGPKGQQGNRGLGFYGVKGEKGDVGQPGPN
{		i	GIPSDTLHP11APTGVTFHPDQYKGEKGSEGEPGIRGISLKGEE
•			GIM
6730	784	1015	NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE
			RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF
6731	 	446	GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS
1 7,51		1 220	LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY
1			
			NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA
	<u> </u>		LIKTARVEINRKDEEI
6732	102	1205	GRWORRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW
1		i	AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN
}		į.	LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE
1			GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE
1			PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR
1	}		POETEEMKTERTTRLOQOHSEOPPLOPSPVMTRRGLRDSHSSEE
]		1	DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR
l		j	_
1			YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG
	ļ	<u> </u>	DKTTRSSSQYIESFW
6733	613	1311	RSCRCVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK
İ			KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI
<u> </u>]	}	QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR
!			VLHRDAILAGEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL
]]]	LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK
l			LLEQEKAYQARKE
6734	100		SAAMFPVFSGCFOELOEKNKSLELVSFEEVAVHFIWEEWODLDD
) 0/34	189	551	
1	I	i	AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalamine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methicnine, N=Asparagine,
I	to first	amino acid	Paproline, O=Glutamine, R=Arginine,
i	amino ació	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotice deletion,
l .	sequence	acqueince	\=possible nucleotide insertion)
	- seguence	:	TLNLRLSGGSKKCVFSGICHRSLVELCEVHLV
6735	280	558	KSRRAGVTKMSNPFLKOVFNKDKTFRI KRKFEPGTORFELHKKA
0/35	200	320	OASLNAGLDLRLAVOLPPGEDLNDWVAVHVVDFFNRVNLIYGTI
1		İ	XDGCT
6736	195	808	MNYELNFKREMPNIKSLGLTNLNFLLKKLSSVLPLITDYVYFEN
6/36	195	808	SSSNPYLIRRIEELNKTASGNVEAKVVCFYRRRDISNTLIMLAD
l	1		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1	}		KHAKEIEEESETTVEADLTDKOKHQLKERELFLSRQYESLPATH
	1		1RGKCSVALLNETESVLSYLDKEDTFFYSLVYDPSLKTLLADKG
			EIRVGPRYQADIPEMLLEGTFFCVFAVL
6737	150	1209	PVIMPLHFSPGDIVRPSCCVSSSPKLRANAHSRLESYRPDTDLS
			REDTGCNLQHISDRENIDDLNMEFNPSDHPRASTIFLSKSQTDV
			REKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTIK
			CVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPPDYDKHN
1	1 .	J	PEQKQIYRFVRTLFSAAQLTAECAIVTLVYLERLLTYAEIDICP
	1		ANWKRIVLGAILLASKVWDDQAVWNVDYCQILKDITVEDMNELE
			ROFLELLOFNINVPSSVYAKYYFOLRSLAEANNLSFPLEPLSRE
			RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLFRWSPAIIS
6738	148	653	CACAEOPARAEVGAATALPVRWASGEM.PSGSLAVFLAVLVLLL
			WGAPWTHGRRSNVRVITDENWRELLEGEWMIEFYAPWCPACQNL
1		i i	QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHC
			KDGEFRRYQGPRTKKDFINF1SDKEWKS1EPVSSWF
6739	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLOKKLAETEKRCALLAAQ
1	}		ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
i			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
i			REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
<u> </u>			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6740	3	631	SWPDMAEEEVAKLEKHIMLLRQEYVKLCKKLAETEKRCALLAAQ
1	1		ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
ł	İ	1	VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
1	į		REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
670	343	ļ	TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6741	141	960	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
1	l .	i	HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
			WDLRSRNLOCORIFOVNAPINCVCLHP%QAELIVGDOSGAIHIW
	<u> </u>		DLKTDHNEOLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
			PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP
6742	141	960	PLTLPFSSRARAGHTMNTSPGTVGSDPV:LATAGYDHTVRFWQA
0/4%	141	360	
]			HSGICTRTVQHQDSQVNALEVTPDRSMJAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
		!	
1			WDLRSRNLQCORIFOVNAPINCVCLHPNOAELIVGDQSGAIHIW
1			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
1		}	PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
6242	 	415	LIPKTKIP
6743	1	412	MHSTODKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK
1		İ	ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLOTOFRN
1			FAEGQETKPKYREILSELDEHTENKLDFLDFMILLLSITVMSDL
	<u> </u>	1	LONIR
6744	95	1343	RTPARNRCAGCEVLSRFSSPNKASSFALÇSAGGGLPAVRALRRD
	1		ROKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQEELT
1	1		DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT
1			LSNEEHFQEPDCSLEAQPKYVRGGKRYGLRSLPEFQESVEEFPE
į.	J		VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLRFWNP
1			DDLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI

			· · · · · · · · · · · · · · · · · · ·
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
!	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acic	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
		1	CEQYGLONVDGEMLEEVFHNLDPDGTMSVEDFFYGLFKNGKSLT
1			PSASTPYROLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVFSCL
1		}	DDGMGHASVERILDTWQEEGIENSQEILKALDFGLDGNINLTEL
	ļ		TLALENELLVTKNSIHQACI
6745	1	588	TFRDQGWAQRRRWLLGCASWESWEAAIAAGPGLPSSTARQQNNP
1		,	AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP
			ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNKWTC
ĺ		1	PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMRAHI
		ļ	RTCOKYIDKYGPLOELEETA
6746	110	492	GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFCTTEI
			SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCEKMA
6747	 	 	VEFGNOLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN
6747	247	484	EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLSVGH
6748	201	665	QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC MTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENFRNL
6/48	201	000	LSVGNOPFHOTFHFLGKEKFWKMKTTSQREGNSGGKIQIEMET
}]		VPEAGPHEEWSCOOIWEOIASDLTRSONSIRNSSOFFKEGDVPC
ł	1		QIEARLSISXVQQXPYRCNECKQ
6749	95	719	REVKGGDGVCPRARGSPQSQGFPSCAGGGEGLQQSGEALDGAM
0143	35	119	SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFDKAF
1			VDVDLLLGEIDPDOADITYEGROKMTSLSSCFAQLCHKAQSVSQ
1		Î	INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQLQL
}	1	1	HAKTGOSADSGTIKAKLSGPSVEELERELKAN
6750	3	426	SCESRRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRATMGT
			TAPGPIHLLELCOCKLMEFLCNMDNKDLVWLEEIQEEAERMFTR
l	1	İ	EFSKEPELMPKTPSOKNRRKKRRISYVODENRDPIRRRLSRRKS
1)	}	RSSQLSSRR
6751	152	1417	PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIV
		İ	NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEML
}	}	}	QHAFEGYNVC1FAYGQTGAGKSYTMMGKQEKDQQG11PQLCEDL
1			FSRINDTINDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
	[1	HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS
1	1		SRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADST
])	1.	GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKTD
	1		FIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLR
i .		1	YADRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGD
	 		ITDMTNALVGMSPSSSLSALSSRNV
6752	24	1834	RNCVPPLGCYRSRVKFHSDIKMQYSHHCEHLLERLNKQREAGFL
1	1	1	CDCTIVIGEFOFKAHRNVLASFSEYFGAIYRSTSENNVFLDOSQ
}			VKADGFQKLLEFIYTGTLNLDSWNVKEIHQAADYLKVEEVVTKC
	1	l	KIKMEDFAFIANPSSTEISSITGNIELNQOTCLLTLRDYNNREK
1	{	1	SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKTVQY
}	1	}	PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE
į.	1		NSGEELDORYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV
1			CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF
1	-	1	HSRMHHGEEKFYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR
}	1)	CGORFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR
[1		
}	1	1	KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED
}	}	J	HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV
	 	 	TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY
6753	2	1305	VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS
}		ļ	PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGFPAAG
	1	ļ.	SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV
1	1	1	AHPGPPPASSOTPAPEHDKAANKMPLAOKPALAPKPTSOTPPAS

CEO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	beginning		
ID NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
) NO:	location		
}		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	Labeucine, Mamethionine, NaAsparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	<u></u>	\=possible nucleotide insertion)
1		,	PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRRPPSPP
İ	i	İ	GPEERKGQKRDEEEEATERKPASPPLPATQOEKPSQTPEAGRKE
1		}	KPMLQSRHSLDGSKLTEKVETAQPLWITLALQKQKGFREQQATR
1			EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALP
1			EEKRPETAVSRLERREQLKKANTLPTSVTVEISYSSPAAPLVKE
l			VSKRFSSPDDAPVSSEPAWLALAKRKAKAWSDCPLIIK
6754	2	413	J VRRRRRRLGGPEVNTMSSLHKSRIADFODVLKEPSIALEKLRE
1.		ſ	LSFSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKQRELYAQ
1		}	FLREMIIOPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD
1		İ	NEVLL
6755	298	1343	PGLQLQVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG
			CGNGTGLRNRNGSAIGLPVPPITALITPGPVRHCQIPDLPVDGS
	<u> </u>		LLFEFLFFIYLLVALFIQYINIYKTVWWYPYNHPASCTSLNFHL
	1	1	1DYHLAAFITVMLARRLVWALISEATKAGALSMIHYMVLISARL
1	!		VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYPFGVYVPLCCFHQ
	l		DSRAHLLLTDYNYVVOHEAVEESASTVGGLAKSKDFLSLLLESL
ł	ļ		KEOFNNATPIFTHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS
ĺ			LFSAYYVAFLPLCFVKVSGYLTFMCFLDLCVNYINWVFLV
6756	180	754	
1 0.50	100	131	LRSLQPOPPGLKQSFCLRVLGLQTGATTPGLRDLTCKELIILTE
į	ļ	[REACKRKKRKEKESGMALTOGPLTFRDVAIEFSQEEWKSLDPVQ
			KALYWDVMLENYRNLVFLGKDNFALEVKICFRVFLYFLCCLSWE
1	į.		PFHYLTETEALLTHK
6757	2	459	NSRVEAPEAHSRESOGSDAMRKHLSWWWLATVCMLLFSHLSAVQ
1 0.3.	, -	433	TRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRKLDID
	1	İ	FGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ
l	l	1	AANQGEFQKPDNKLHQQVLW
6758	<u> </u>	1008	ASGPELPGRRFRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR
(0,30	1	(1000	RVPSLAOLGHSEAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPPS
ł		<u> </u>	LPPSFRRNMANNSPALTGNSQPQHQAAAAAACQQQQCGGGGATK
1	ļ		PAVSGKOGNVLPLWGNEKTMNLNPMILTMILSSPYFKVQLYELK
1	ļ		TYHEVVDEIYFKVTHVEPWEKGSRKTAGQTGMCGGVRGVGTGGI
	ĺ	į	VSTAFCLLYKLFTLKLTRKQVMGLITHTDSPY1RALGFMYIRYT
1	1		OPPTDLWDWFESFLDDEEDLDVKAGGGCVMT1GEMLRSFLTKLE
	l		OPPIDEMENT OF THE PROPERTY O
6759		513	RKHNFHSLDGTSTRAFHPOTGLPLLSSPVPORKTOSGCFDLDSS
0/39	ī	213	LLHLKSFSSRSFRPCLNIEDDPDIHEKPFLSSSAPPITSLSLLG
			NFEESVLNYRFDPLGIVDGFTAEVGASGAFCPTHLTLPVEVSFY
1			SVSDDNAPSPYMGVITLESLGKRGYRVPPSGTIQVVCVL
6760	336		·
6/60	239	606	VISKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGIT
	})	AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLE
			VLESQLSEGSQKHASLQKSIEKAKIGRCETEERT
6761	29	1733	ERTLRGLEEVAAPSDVADAAVSRRGRCCCCLHCTQTQVAQDCPS
	Į.	!	SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALAGLVACNP
)	j		NLCLLOGHRVALRSDLDSLKGRVALLSGGGSGHEPAHAGFIGKG
	1		MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLLIVKNYTGD
1	[RLNFGLAREQARAEGIPVEMVVIGDDSAFTVLKKAGRRGLCGTV
	İ	1	LIHKVAGALAEAGVGLEEIAKQVNVVTKAMGTLGVSLSSCSVPG
1	1	1	SKPTFELSADEVELGLGIHGEAGVRRIKMATADEIVKLMLDHMT
			NTTNASHVPVQPGSSVVMMVNNLGGLSFLELGIIADATVRSLEG
1	}	1	RGVKIARALVGTFMSALEMPGISLTLLLVDEPLLKLIDAETTAA
		l	AWPNVAAVSITGRKRSRVAPAEPQEAPDSTAAGGSASKRMALVL
1	{	}	ERVCSTLLGLEEHLNALDRAAGDGDCGTTHSRAARAIQEWLKEG
1	1	1	PPPASPAQLLSKLSVLLLEKMGGSSGALYGLFLTAAAQPLKAKT
	,	ř .	SLFAWSAAMDAGLEAMQKYGKAAPGDRTMLDSLWAAGQBL

	Drodieted	Trundiated and	Limina rold compart consists and account of
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalenine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine,
	1	to first	
	corresponding		L=Leucine, M=Methionine, N=Asparagine,
	to firs:	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino ació	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion;
6762	3	613	ASTISWRLCVAGAEARRPVPVAGERAGGGAMWFMYLLSWLSLFI
			OVAFITLAVAAGLYYLAELIEEYTVATSRIIKYMIWFSTAVLIG
			LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG
		į	LVVVNHYLAFQFFAEEYYPFSEVLAYFTFCLWIIPFAFFVSLSA
			GENVLPSTMQPGDDVVSNYFTKGKRGK
6763	2	760	SGPDFPGRRFRGCCCVRPPAGAGMELGGHWDMNSAPRLVSETAE
	j		RKQEQKTGTEAEAADSGAVGARRFLLCLYLGGFLDLFGVSMVVP
		1	LLSLHVKSLGASPTVAGIVGSSYGILQLFSSTLVGCWSDVVGRR
		1	SSLLACILLSALGYLLLGAATNVFLFVLARVPAGIFKHTLSISK
		1	ALLSDVVFEKERPLVIGHFNTASGVGFILGPVVGGYLTELEDGF
	[YLTAFICFLVFILNAGLVWFFPRREAKPGSTE
6764	80	438	LKKMDTMMLSVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFR
			KKWORTDHELGKYKDLLMKAETERSALDVKLKHARNOVDVEIKR
		1	RORAEADCEKLERQIQLIREMLMCDTSGSIQ
6765	3	550	AKYSRVDHFCRRCRAVARAPRFLLQFPSGPSRHFLAACVARWL
)		RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS
		ì	NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLPGEVTETE
	1	1	VIALGLPFGKVTNILMLKGKNQAFLELATEEAAITNGNYYSAVT
			PELRNO
6766)	1287	EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGVR
		ţ	AVLSLCOOTSRSOPPVRAFLLISTLKDKRGTRYELRENJEOFFT
		İ	KFVDEGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN
			VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHL
		1	QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ
		1	ELNLNDNHLESFSVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ
			LCELKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF
	İ	ł	RNLSLEYLDLFGNTFEQPKVLPVIKLQAPLTLLESSARTILHNR
			IPYGSHIIPFHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV
		ļ	AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI
6767	336	919	APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV
			GRLOSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY
			ROPLPOPTCDPEQLGLRHAQKAHOLQSDVKYKSDLNLTRGVGWT
			PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV
			NPDATEILHVKKKKALLL
6768	2	363	PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE
	1	1	LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV
	1	1	ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL
6769	284	396	MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD
6770	3	397	ORNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK
	1		ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF
			KIROGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS
6771	3	378	APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR
	Į.		WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM
	1		QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG
6772	1	1400	AAAFLOGMTVNGFINTVITSL\ERRYDLHSYOSGLIASSYDIAA
,	1		CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG
	1		P*+GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGOFL
	1	}	HGVGATPLYTLGVTYLDENVKSSCSP1YIAIFYTAAILGPAAGY
	1		LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT
•	1	1	AVPILGYPROLPGSORYAVMRAAEMHOLKDSSRGEASNPDFGKT
	1		
	1		IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES
	1		QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK
	1	}	FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL
	1	-	TAPCNAACSCOPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG
	1	1	QKVYRDCSCIPQNLSSGFGHATAGKCTST

SEC	Predicted	Predicted end	That are the second and the second are the second and the second are the second a
ID		nucleotide	Amino acid segment containing signal peptide
NO:	beginning nucleotice	location.	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	1		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Iscleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acić	secuenc∈	Codon, /=possible nucleotide deletion,
	seguence	ļ	\=possible nucleotide insertion)
6773	1	630	PWEAPKEHKYKAEEHTVVLTVTGEPCHFPFQYHRQLYHKCTHKG
İ	1		RPGPQPWCATTPNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT
			CVNMPSGPHCLCPQHLTGNHCQKEKCFEPQLLRFFHKNEIWYRT
1	<u>i</u>]	EQAAVARCQCKGPDAHCQRLASQACRTNPCLHGCRCLEVEGHRL
1			CHCPVGYTG?FCDVGE*GSGASRRPAPRWDGLAR
6774	146	389	LTELSDQQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIISS
ĺ	İ	1	GLRIGFLTGPKPLIERVILHIOVSTLHPSTFNQLMISQ
6775	104	614	TCPSQLRVLTARGGRRAPSPOLWTLVLALIEEKWRSHRILRMNS
1		Ì	GRPETMENLPALYTIFQGEVAMVTDYGAFIKIPGCRKQGLVHRT
			HMSSCRVDKPSEIVDVGDKVWVKLIGREMKNDRIKVSLSMKVVN
1		1	QGTGKDLDPNNV\SLSKKRGGGDPSRITLGRRSPLRLS
6776	3	1108	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPOWQLLH
1	,	1	LNGTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSQSL
1			: TSVAKFVFMAGMMVGGILGCHLSDRFGRRFVLRWCYLQVAIVGT
1		,	CAALAPTFLIYCSLRFLSGIAAMSLITHTIMLIAEWATHRFOAM
			GITLGMCPSGIAFMTLAGLAFAIRDWHILOLVVSVPYFVIFLTS
1			·
		1	SWLLESARWLIINNKPEEGLKELRKAAHRSGMKNARDTLTLEIL KSTMKKELEAAOKKKPFLGERLHMPNICKRISLLPFTKFANFMA
1		į	1
1		1	YFGLNLHG/LKHLGNNVFLLQTLFGAV/TPPGQLVLHLGHWGSG
			RVSSRGRVNCLGLFVLQVW
6777	779	63	CFFHGPAWRDCEVRATFAKKOGOSGIISCJAFSPAQPLYACGSY
		1	GRSLGLYAWDDGSPLALLGGHQGGITHLCTHPDGNRFFSGARKD
1	ŀ		AELLCWDLROSGYPLWSLGREVTTNORIYFDLDPTGQFLVSGST
1			SGAVSVWDTDGPGNDGKPEPVLSFLPQKDCTNGVSLHPSLPLLG
	}		HCLPVSVCFLSPTESGGRRRGAGPSLGSPRRHVHLECRLQLWWC
	ļ	L	GGGARLQHP++SPRARKGR
6778	311	805	IQSITDESRGSIRRKNPANTRLRLNVP\EETAGDSE/ERSPEEE
1		1	VQADPRIRSASPKCPTSSPFPKGRSPEGEGET\DPEKVHFHPGP
1	1		KDKSVAEKN/KGP/SPVSSEGIKDFFSMKPEWENLNQSNVRRMH
			T\AVRLNEVIVKKSRDAKLVLLNMPGPPRNRNGDENY
6779	2	535	RALRROPRLLAANGIEPESMAISEPIKGSKKPCVNKEELALKKP
1	1		MAKCAWKGPREPPQDARAEAESPGGASESDQDGGHESPPKKKAV
1			AWVSAKNPAPMRKKKKVSLGPVSYVLVDSEDGRKKPVMPKKGPG
1	1	ĺ	SRREASDQKAPRGQCPAEATASTSRGPKAKPEGSPRRATNESRK
L			ν
6780	3	403	HEVNDNKPEININLMSPGKEEISYIFEGDFIDTFVALVRVQDKD
1	}	1	SGLNGEIVCKLHGHGHFKLQKTYENNYLILTNATLDREKRSEYS
1	}		LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE
<u></u>	1		K
6781	1	1269	AFTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPELSEVS
1			SNVAPSIPPVMSRPVSSSSISTFLPPNQITVFVTSNPITTSANT
1			SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI
1	1	{	TPVFINSSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL
1	1		HIPONIKESSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVOLP
1		1	SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ
1			STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGOILLTKAC
l	1	l	KKVTGSLEKGEEQYGADGETEGCGLDTTAPGLMGTEQLSTELDS
1	ļ.	1	KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT
	1	!	
6782	 	1222	LVPSELISAVPTTKSNEGGIASESLAG
0/62	3	1327	RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS
1	1		NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKT1PTQQPPTK
1	1]	VPPERPPPPKLSATRRSNKKLPFNRSSSDMDLQKKQSNLATGLS
1	1	1	KAKSQVFKNQDPVLPPRPKPGHPLYSKYMLSVPHGIANEDIVSQ
1	1		NPGELSCKRGDVLVMLKQTENNYLECQKGEDTGRVHLSQMKLIT
L	!	l	PLDEHLRSRPNPFSPPKAPSHAOKPVDSGAPHAVVLHDFPAEQV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histiding, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, K=Methionine, N=Asparagine,
	to first	amino acid	· · · · · · · · · · · · · · · · · · ·
1	!		P=Proline, G=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, %=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptopher, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DDLNLTSGEI\'YLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI
į			PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
		<u>.</u>	LKEYVNEEWALGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV
1	į	1	PLKTKKEDSGENSQVNSLPAEWCEALHSFTAETSDDLSFKRGDR
1	1		I
6783	3	1750	SYHHHHAQQSA.A.ASPNLTASQKTVTTTSMITTKTLPLVLKAATA
6/83	3	1/50	
1	l		TMPASVVGQRFTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
l	i		GPGAEAVQIVAKKTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
1			LPOVRPKPVACHNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
ł			PTSQNSIHPVKVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
1	1		QTVQLSKPSLERQTVKSHTETDEKQTESRTITPPAAPKPKREEN
i	l		PQKLAFMVSLG1.VTHDHLEEIQSKRQERKRRTTANPVYSGAVFE
	1		PERKKSAVTYLMSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
f	(1	SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
1	1	1	RKSGOLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
j			KEEAIPNPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
ļ		,	LEOKVKOLSNS SKCMEMKNTILAROKEMHSSLEKVKOLIRLIH
1	1		GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSOSCT
1	İ	l .	
			ANCNOGEETK
6784	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
1			TMPASVVGQRFTTAMVTAINSQKAVLSTDVQNTPVNLOTSSKVT
1			GPGAEAVQIVAENTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
1			LPOVRPKPVACNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
1			PTSQNS1HPVR\\VNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
	1		QTVQLSKPSLEROTVKSHTETDEKQTESRTITPPAAPKPKREEN
ļ			PQKLAFMVSLG1.VTHDHLEEIQSKRQERKRRTTANPVYSGAVFE
1	1		PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
			SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
	1		RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMW1CPRCQDOMLK
1			KEEAI PWPGTLAJ VHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
ļ	İ		LECKVKQLSNS: SKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
	1		GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSOSCT
			ANCNOGEETK
6785	1 1	528	LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR
1 6/63	1	320	LKATOCEDLLS(AKSGKFNPHVHVEYEWNLRQEEIDESDDDLDD
			= · · · · · ·
	1		KPSPVKKERSPkPOSFCHSSSISPQDKLALPGFSTPRDKQRLSY
		<u> </u>	GAFTNQIFVSTSTDSPTSPTTEAPPLPPRNAGKGPTGPPITPHR
6786	182(1397	RSPKVLVLAPTAELANHVSRDFKDI\TRKLTVARFYGGTSYQSQ
1			INHIRNGIDILVGTPGRIKDHLQSGRLDLSKLRHVVLDEVDQML
1	ļ		DLGFAEQVED1: HESYKTDSEDNPQTLLFSATCPQWVYTVA\KK
	1	1	YMKSRYEQVDLPGKMTQKAATTVEHLAIQCHWSQRPAVIGDVLQ
1	1		VYSGSEGRAIIFCETKKNVTEMAMNPHIKQNAQCLHGDIAQSQR
]		EITLKGFREGSFKVLVATNVAARGLDIPEVDLVIQSSPPQDVES
		ļ	YIHRSGRTGRAGETGICICFYQPRERGQLRYVEQKAGITFKRVG
1			VPSTMDLVKSKEMDAIRSLASVSYAAVDFFRPSAQRLIEEKGAV
1			4
1		Į	DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLEEIQDVSC
	1		AWKELNRKLSSNAVSQITRMCLLKGNMGVCFDVPTTESERLQAE
1			WHDSDWILSVPAKLPEIEEYYDGNTSSNSRQRSGWSSGRSGRSG
			RSGGRSGGRSGHOSRQGSRSGSRQDGRRRSGNRNRSRSGGHKRS
1			FD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS
1			SVWN
6787	264€	2270	PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF
1			FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI
1	-		LVFLVEMGFHHVGOAGLKLLTL\VIHPPWPPKVLGLQT
6788	16	936	GGTVDLR\DMLAVSVLAAVRGGR/ATVRRVRESNVLHEKSKGKT
1 5,00	1	336	REGAEDKMTSGDVLSNRKMFYLLKTAFPSVQINTEEHVD\ELDQ
L		!	VEGUTDUALISONA ESMANGEL LEDVINES AND CHANGE LAND (PEDIÓ

Deginning	CEO.			
No: location corresponding to first amino acid residue of sixt amino acid residue of samno acid residue of samno acid sequence solvente, whethionine, N-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, Oscilutamine, R-Asparagine, P-Proline, V-Valine, W-Tryptophan, V-Tyrosine, X-Uuknovn, *-stop Coden, /-possible nucleotide deletion (Coden, /-possible nucleotide deletion) (P-Proline, X-Valine, W-Tryptophan, V-Tyrosine, X-Uuknovn, *-stop Coden, /-possible nucleotide deletion) (P-Proline, X-Valine, W-Tyrosine, X-Uuknovn, *-stop Coden, /-possible nucleotide deletion) (P-Proline, X-Valine, W-Tyrosine, X-Uuknovn, *-stop Coden, /-possible nucleotide deletion) (P-Proline, X-Valine, W-Tyrosine, X-Va	SEC	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence Septence		-		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Leibeucine, M=Methionine, N=Asparagine, amino acid residue of amino acid residue of amino acid sequence Seserine, T=Threcnine, V=Valine, amino acid sequence Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, T=Threcnine, V=Valine, Seserine, V=Threcnine,	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid sequence sequ	İ			
amino acid residue of amino acid sequence W-Typtophan, Y-			, ·	
meinde of amino acid sequence Sequence			1	
amino acid sequence Codon, /=possible nucleotide deletion Lopossible nucleotide filetion EVILMGS-DS-GTPKGK-LLPKEVFSR/RVLLSGLTPLDATQE\ FTEDLSKLYUTTMVCUAVNCKPMLGVIHKPRSSY-ANAMVDGGS NVAMSSYNKETREJ WESHSGANKVALDITFENGTTIPAGG AGYKVLALLDVPDKSGEKADLYHHTTIKONDICAGNALLKALG GENTTLSGERISTSCSGLGSGLASI RRNNQALVEKHLPDLEKT GHR 6789 2 678 GNGINVLKIAPESAIKFNAYEQIKRLWW-FGDS-GF/YERLVA GSLAGAIAOSSIY PMEVLKTRMALRKTGOYSGMIDCARRILARE GVAAFYKGYVPMHGITIFYAGIOLAVYETLGNAMLQHAVINSAD PGVFVLLACCTHSSTCGOLASYPLAUNTRWOAQASIEGAPEVT MSSL-KRYKLYPKHGITIFYAGIOLAVYETLGNAMLQHAVINSAD PGVFVLLACCTHSSTCGOLASYPLAUNTRWOAQASIEGAPEVT MSSL-KRHILETEGA-GRIVAGLAPPFMKVIPAVSISTVVVENLKI TLZVQSR 4068 APPAGRERMGAAPPRAGGGAALLIKTVSSCLCEANTAPSTGOKED HYORLQVBFGNIKAPENGGGAALLIKTVSSCLCEANTAPSTGOKED HYORLQVBFGNIKAPENGGGAALLIKTVSSCLCEANTAPSTGOKED HYORLQVBFGNIKAPENGGGAALLIKTVSSCLCEANTAPSTGOKED HYORLGVBFGNIKAPENGGAALLIKTVSSCLCEANTAPSTGOKED HYORLGVBFGNIKAPENGGAALLIKTVSSCLCEANTAPSTGOKED HYORLGVBFGNIKAPENGGAALLIKTVSSCLCEANTAPSTGOKED HYORLGVBFGNIKAPENGGAALLIKTVSSCLCEANTAPSTGOKED HYORLGVBFNIKAPSTGOKENFORGENITAPSTGOKED HYORLGVBFNIKAPSTGOKENFORGENITAPSTGOKED HYORLGVBFNIKAPSTGOKENFORGENITAPSTGOKENSTGOKENFORGENITAPSTGOKEN KPHODONINAPSCHICHTIAPVILLYBENGAMSHANIKAPSTANDEN EGRICALT EUVICSYNADVINFERVOKULFYFRNIKAMTLIKDSWQHFR TNOEPSYLDLDLET ITGGIPFSGKRESSRKNYKGMESSINTMG WINTDLARRKLEPSNVGNLSFSCVEPYTVVPFFNIKTSVLEVPG RINCOLFSVFFORTHNONGLLUFFBRANDIANUTELDLTSSKYG VHINTITOTANGOIDISSGSGLNOGOMEWFLIAKENFATLITIOG DEASAWTNSPLOVKTERSYFFORGHENITAPSTLEVPG RINCOLFSVFFORTHNONGLIMFSRANDIADHANIKAPSHANDAFORGHANIKAPSTANDESFORGHANIKAPSHANDAFORGHANIKAPSHANDAFORGHANIKAPSHANDAFORGHANIKAPSHANDAFORGHANDAFO				The state of the s
Sequence V=possible muclectide insertion			1	
EVILMES DS-GYPKGN-LIPREVESR/RVILSGLTPILDTOCK PTEDLSK\VTINCVANNEKMENG HERESYTANBAWDGGS NVKARSSYNEKTPRI VVSRSHEGRWKOWALOTFGROTT I PAGE AGYKVLALLLUP PBKSOEKALDYTHVYTIKRODI CAGNATIKALG GEMTTLSGEEISYTCSDGLEGGLASIRMHIGOLIVRIKPUEKK CHR GNGINVLKIAPESAIKFMAYEQIKRLVW-*PGDS-GF/YERLVA GSLAGAIAOSSIYPHEVLAKTRMALRKTGOYSGMILDCARRILAGE GVAPAYKGYVPMINGLI PYNAGILAVYETLKANAULHYANNSAD PGVPULLACGTMSSTCGOLASYPLALVETRMALAGHAVNSAD PGVPULLACGTMSSTCGOLASYPLALVETRMALAGHAVNSAD PGVPULLACGTMSSTCGOLASYPLALVETRMALAGHAVNSAD PGVPULLACGTMSSTCGOLASYPLALVETRMOAQASIEGAPSTV MSSLFRHILERTEA-GGLYRALLAPPKKYIPANSISTYVYPRIKI TLGVQSR 6790 2 4068 APPAGRRHMQAAPRAGCGAALLENIVSSCLCRAWTAPSTSOKCD EPILVSGLPHVAPFSSSSISGSYSGVAKINKRGGAGGKSPGDSD HYOMLQUPFGRIKAGISAITQGRSSSDWTOYMAN BYGTGRIN KPYHODGRI MAPPGRI INSDOVURHELQHP I IARVYRI VIPLIMM EGICAL PLVGGCSYMADIVIN PGROWLYD PYRENKWHCTLKODY ALAPKTSSEGVILHGEGOGGDYITLELKKAKLVILSLNLGSNQL GPIYGHTSYWTOSILLDHHMIBWVIERGGRSINITLDRSKNGMFT TINGEPDYLLDLYEI TPGGIP PSGRSSSSKRINGKGMESINTIN WINITDLARKKLEPSINGKHSSSCVEPTTYDVFFRATSYLEPP READER FRANCHING FRANKHSTEN STANDEN WINITDLARKKLEPSINGKHSSSSKROPHEN PRATSYLEPP READER FRANKHSLOD SAGSGLINGGOMEVRILAKENPAILTID DEASAVARTHSPLOV KYTEKEY FFGEFILMONINS-HSEN-LOPS-GFGC MOLIOVDDOLAVILY BYAQKRGSFANVSIDUCAI I DRCVINKHS VYHINITOTIKNSOID I SSGSGLINGGOMEVRILAKENPAILTID DEASAVARTHSPLOV KYTEKEY FFGEFILMONINS-HSEN-LOPS-GFGC MOLIOVDDOLAVILY BYAQKRGSFANVSIDUCAI I DRCVINKHS VYSYTOLAVSANDGI SASITISABEYCGOYYSYFCKMSKILL NTPOSSFYTHWVCKANSKHYWGGSGFGIOKCACGIERNCTOPH YYCNCDATYKORKBOFT-FRANKILD-FROMFYTOKHENDAY YYCNCDATYKORKBOFT-FRANKILD-FROMFYTOKHENDAY YYCNCDATYKORKBOFT-FRANKILD-FROMFYTOKHENDAY YYCNCDATYKORKBOFT-FRANKILD-FROMFYTOKHENDAY YYCNCDATYKORKBOFT-FRANKILD-FROMFYTOKHENDAY YYCNCDATYKORKBOFT-FRANKILD-FROMFYTOKHENDAY YYCNCDATYKORKBOFT-FRANKILD-FRANKINGT-FRANKILD SAFTYNTDDORRAMAROTINAS-HVYHIGGELVESNCGASFALTE-FRANKINGT-FRANKILD GTREPYNI DVDRRMANAROTINAS-HVYHIGGELVESNCGASFALTE-FRAN SGCGGGCTSYGTTCSNGGCGGGFGCT-GRONG-FRANGATH-FRANKILD FEIRPSFTTATPGRPTGCGA-FRANGATH-FRANGATH-FRENKINGT-FRANKINGT-FRANKILD FRANKSTHANDAY-FRA			sequence	
FTEDLSK, YVTTMVCVAVNCKPMLGVIHKPSTYANAMYDGE NVKARSSYNKETPI VVSESHSGAVKVAVALOTESTYOTTI PROG AGYKVLALLDUPDKSOBRADLYIHVTYI KRNDI CAGNAILKALG CHMTTLSGEEI SYTESDI EGGLLASI RWHNIGALVRKLPDLEKT CHK 6789 2 678 6NGINVLKIAPESAI KFMAYEQIKRLW** FEDS*GF/YERVJC GSLAGAIAOSSI YPEVLAKTRMAKTGOY SGMILDCARRILARE GVARFYKGYVPHMLGI TPYAGIDLAVYETLYANAMLQHYAVNESA PGVPULACCTIMS STCGOLASYPLALVETMYAQASI EGGPEVT MSSLFKHI LRTEGARGUKGLAPPHKVI PAVSI SYVYYENLKI TLAVOSR 6790 2 4068 APPAGRRHMOARPRAGCGRALLKIVSSCLCRAWTAFSTSOKCD EPILVSGLPHAPESSSSI SGSYSPOYAKI NKRGGAGGKSPDSD HYONLOVPIGNKOI SALATOGRISSSUMYTOYRMI. SDTGRNN KPHODENI WAPFERI INSOCVERHELQIPP I TARYVRI VPLDMEN EGG I EGLR LEVYGSCYMADI VINDENVUPLYBERKNEKTLKDVI ALMFKTSSEGVILLEGGGOGDYTTLELKKAKLVLSINLGSWOL GPI YGMTSWTTGSLEDHHMHSVLVI ERGGGSI DHUSSWOHFR TNGEPDYLDLDVEI TFGGI PPSGKRSSSS RNFKGCMESINTING VNI TDLARKKLGEPSNVGLIASFECOGOBYTTLELKKAKLVLSINLGSWOLF FUNGERSVARDVINDENVENSTERPRONICH STERVETYPVEV PFARTSYLEVYG RINODLFSVSFOR RWHPNGLLVFSHFADNIGNVEI DLTSSKVG GEN STATTNSFLOV KYGEKYFFGGFILNOMNSSHSVLOPSFOC MOLIOVDOLVINLY SVAORKOESEANVSIDMCAI IDROVPNICE HGGKCSOTNOSFKCTCGETGYSGATCHNSI YEBSCBAYKILGOF NPYMYADDPOGSGILPLAVYCKUMPEROWEN I TIDROVPNICE HGGKCSOTNOSFKCTCGETGYSGATCHNSI YEBSCBAYKILGOF NPEXYSVTOLVYSASMO ISAITOSAEYCGVYSYFCKMSLL NTPOGSYTYHWVGKANEKPI YWGGSGGIOKCACGIERNCTUPS YYCNCDADYKOMRKEDFILLELKENEVAVVI VEHOVORYVUG SPYPLINDGONHAVTAERNVKOASLOVORLOOGINKAPTELAKHEN SPYPLINDDONHAVTAERNVKOASLOVORLOOGINKAPTELAKHEN SPYPLINDDONHAVTAERNVKOASLOVORLOOGINKAPTELAKHEN SPYPLINDDONHAVTAERNVKOASLOVORLOOGINKAPTELAKHEN SPYPLINDDONHAVTAERNVKOASLOVORLOOGINKAPTELAKHEN ELIYSSTITKAPCILLYISSFTTDELAVLVKPTSSLOI RYNIG GTEEPYNI DUDINANAROPORANTINGENEVIT PSISAITSPSCAKL SVEPLECOGGRNYMAASFPROSSVINAPSCONSTANYDOTTCKKO GTERSTYNTON POR PARTAGRAFINGSTANTING PSI VYCHYDEN SATTURENT TILLFUR PSI VY HLPSSSDTLENSKSLFICKVI ETGG I IDOEI HKYNTOFSGFI SGCSGCTSYGTNCHOGKCLERWTOPS SVEVYDETTSSLOI RYNIG GTEEPYNI DUDINANAROPORANTINGENET TREBRIJATHESMO NSGI I ESSVETNI GNF DWWIGKRGAPUSGVY FTTESMKOHD V EFTYVILMHGONY SWYSYMKKSOTSNITHAVILLAKAGEVU LRHGGNALHODHO		sequence		
NVKARSSYNEKTERI VVERSHEGMIKOVALOTTEGKOTTI I PAGE AGY KVIALLLUP MEKSÖRKALDI HINTYTI KRADI CAMAILKALG CHMTTLSGEEI SYTCSDGI EGGLLAS I RMINIOALVRKLPDLEKT CHK 6789 2 678 GNGINVLKI APESAI KFMAYEQIKRLVW** PGDS*GF/YERLVA GSLAGAI ADOSSI Y PHEVLAKTRMALRIKTGOY SGMILDCARRI LLAG GVARAFKGY VPMILGI I PYAGI LLAVYETI.NAMALDHAVMSAD PGVPULLACGTMSSTCGOLASYPLALVRITRMOAQAS I EGGPEVT MSSLF KHI LERTEGA FGLYKGLAPPHMKVI PAVSI SYTVYPELVI TLAVQSR 6790 2 4068 APPAGRRMQAAPRAGCGAALLKI VISSI CHAWTAPSTSOKCD EPLVSGLPH APPAGRSSI SIGSYSFOYAKI INKRGAGGKSEBISD HYQWLQVDFONKOI SAIATOGRYSSISDWTQYRMI-SYDTGMIK KPHODONI MAR PFRAGCGAALLKI VISSI LUPUNIN-SYDTGMIK KPHODONI MAR PFRAGCGAALLKI VISSI LUPUNIN-SYDTGMIK KPHODONI MAR PFRAGCGAALLKI VISSI LUPUNIN-SYDTGMIK KPHODONI MAR PFRAGCGAALLKI VISSI LUPUNIN-SYDTGMIK KPHODONI MAR PFRAGCGAALLKI VISSI LUPUNIN-SYDTGMIK KPHODONI MAR PFRAGCGAALLKI VISSI LUPUNIN-SYDTGMIK KPHODONI MAR PFRAGCGAALLKI VISSI LUPUNIN-SYDTGMIK-SYD				,
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GHR GNSINVLKIAPESAIKFMAYEQIKRIDW**PGDS*GF/YERIVA GSLAGAIAOSS1YPMEVLKTRMARKTGOYSGMIDCARRILARE GVAAFYKGYVENNIGII IPYAGIDLAVYETLKAMAUQHYANSAD PGVPVILLACCTINS*TCGQLASYILAURETMAQAQASIEQAPEVT MSSLFKHILRTEGAFGLYRGLAPREMKYIPAVSIESYVYYENIKI TLZVQSR 6790 2 4066 APPAGRRAPGAGAALALIKIVSSCLCRAWTAPSTSOKCD EPILVSCLPHVAFSSSSISGSYSFGYAKINKRGGAGKSPSDDD HYQMLQVDFGRRKOISAIATGGRYSSDWYTQYRMINSDTGRNM KPHODGNI WAPFGNINSDGVVERIBLOPFI LARYVRI VPILDMOR GERIFIGIRIEVYGCSYWADVINDFGWVLVPFRNKKMRTLKDVI ALMFKYTSESECVILHGEGOGDYITLELKKAKLVLSINLGSNOL GPIYGHTSWYRGSLADDHHHMSVVERGGGIFFNKKMRTLKDVI ALMFKYTSESECVILHGEGOGDYITLELKKAKLVLSINLGSNOL GPIYGHTSWYRGSLADDHHMSVVERGGGIFFNKKMRTLKDVI ALMFKYTSESECVILHGEGOGDYITLELKKAKLVLSINLGSNOL GPIYGHTSWYRGSLADDHHMSVVERGGGIFFNKKMRTLKDVI ALMFKYTSESECVILHGEGOGDYITLELKKAKLVLSINLGSNOL GPIYGHTSWYRGSLADDHHMSVVERGGGIFFNKYMTATUDRSMOMFR TNGEPDYLDLDYEITFGGIPPGGKPSSSRNFKGCMESINYNG WINITDLARRKKLEPSNVONISPFGCVEPYTYDFARTSYLEVYG RINCOLFSVSFOFRTWNPNGLLVFSHFADNIGNVEIDLTESKVG WHINITOTKMSOIDISSGSGLANGGWHEVEFLAKENPAILTIDG GRANARTINSFFOCVEPTYDFARTSYLEDYSFGC MQLIOVDDOLUNLYEVAGRKPGSFANVSIDMGAIIDRCHIPTSKVG WHINITOTKMSOIDISSGSGLANGGWHEVEFLAKENPAILTIDG GRANARTHSPORTSYNTENDERGARTHANGANIAURA HEGGESTUDSFFOCVETTETTFGGETLOMMNSVLOPSFGCC MQLIOVDDOLUNLYEVAGRKPGSFANVSIDMGAIIDRCHIPTSKVG SNYYHIDPGSGFLGFLKVYCHNTEDKWFI USHDLOMOTPVVG YNPEKYSVTOLUYSASMODISATTSARYETGGATICHSIEYSPCKPNKILGOT SNYYHIDPGSGFLGFLKVYCHNTEDKWFI USHDLOMOTPVVG YNPEKYSVTOLUYSASMODISATTSARYETGGATICHGAIITSCAPSTCHARCH SVGPLKCOGDRNYWNAASFPNPSSYLHPSTFOGETSADISFYFK TLTPMGVPLEMMKEBFI KLELKSATEVSFSTDUCNOPPEUVR SYPPLINDOMHRVAGAALTGARASFTVLHPSTFOGETSADISFYFK TLTPMGVPLEMMKEBFI KLELKSATEVSFSTDUCNOPPEUVR SPPPLINDOMHRVAGAALTGARASATVHOGELVERTGGAFGAGAGG GGGGGGGGGGGGGGGGGGGGGGGGGGGG			· ·	AGYKVLALLDVPDKSQEKADLYIHVTYIKKWDICAGNAILKALG
6789 2 678 GINGINUKIAPESAIKERÄYEQIKELUW* FEDES-GFYYERIJAR- GUARPIKGYVAPINIGIIPYAGIDLAVYETIKNAMLOHYAMNSAD PGVFULLACGTMSSTCGGLASTPILAURTEMQAQASIEGRPVT MSSLFRHILRTEGAFGUKGLARPIMKUIPAVISAD PGVFULLACGTMSSTCGGLASTPILAURTEMQAQASIEGRPVT MSSLFRHILRTEGAFGUKGLARPIMKUIPAVISAY MSSLFRHILRTEGAFGUKGLARPIMKUIPAVISTSYVYENLKI TLZVQSR 6790 2 4068 APPAGRRINDAPPAGCGALLLIKIVSSCLCRAWTAPSTSOKCD EPLVSGLPHVAPSSSSISGSYSFGYAKINKRGGAGGKSPSDSD HYWOLQVDFGRIKOISALATGGKYSSSDWYTGYRIN-SDYDGRIN KPYHOLGRI WAPPGRINDSDCVARELGHPI LARVYRI VPLDIMG EGRIGLRIEVVGCSYWADVINPGGIVVLPYRFRIKKKTLDVI ALMFKTSSESCVILHGEGGGOGYTILELKKAKULSINLGSKOL GPIYGHTSVMTGSLLDDHHHHSVVIERGGRSINLTDLDRSMGMER TNGEFDYLDLDLYGIFTSGGPSSKSSSKSKFKGKGMSINYNG WINTDLARRKLEPSNVGNILSPSCUEPYTY PVFFRATSYLEVPG RIKODLFSVSFG RTWINNGLLDYSHFADMLGNVEIDLTESKVG VHINTOTKMSDID ISSOSGLANGGOMHEVER LERPALLTIDG DEASAWRTINSFLOVKTGKKYFGGFLINDKINNSHSVLOPSFGGC MOLIOVDDOLUNILYEVAGRKYBGFANVSIDMCKIPALTIDG DEASAWRTINSFLOVKTGKYFTGGFLINDKINNSHSVLOPSFGGC MOLIOVDDOLUNILYEVAGRKYBGFANVSIDMCHIDATTSKVG YNYAUDPDGSFLGFLKVYCOMTEDWATI SEPSCEAYKHLGOT SNYYWIDPDSSPLGFLKVYCOMTEDWATI SEPSCEAYKHLGOT SNYYWIDPDSSPLGFLKVYCOMTEDWATI SEPSCEAYKHLGOT SNYYWIDPDSSPLGFLKVYCOMTEDWATI SEPSCEAYKHLGOT SNYYWIDPDSSPLGFLGFLKVYCOMTEDWATI SEPSCEAYKHLGOT SNYYWIDPDSSPLGFLGFLAVVYCOMTEDWATI SEPSCEAYKHLGOT SNYYWIDPDSSPLGFLGFLAVVYCOMTEDWATI SEPSCEAYKHLGOT SNYYWIDPDSSPLGFLGFLAVVCOMTEDWATI SEPSCEAYKHLGOT SNYYWIDPMSSCHIGKTSTAGFLGGSEAL SUGPLKCOGORNYWNAASFFNYSSYLHFSTFGGETSAD ISYFIK TLTPMGVFLERMKGEDFIKLEKASTEVSFSTOVONGPVEIVVR SPPTIMBODHHRVTAERNVKOASLQVIRKDLOOIRKAFTEGHTAL ELYSOLFVGGGGOGGFLGGLRAWVUTPOUTDGGSEAKL SUGPLKCOGGGOGFLGGLRAWNOVLOUGTDROGSEAKL SUGPLKCOGGGOGGFLGGLRAWNOVLOUGTDROGSEAKL SUGPLKCOGGGOGGFLGGLRAWNOVLOUGTDROGSEAKL SUGPLKCOGGGOGGFLGGLRAWNOVLOUGTDROGSEAKL SUGPLKCOGGGOGGFLGGLRAWNOVLOUGTDROGSEAKL SUGPLKCOGGGOGGFLGGLRAWNOVLOUGTDROGSEAKL SUGPLKCOGGGOGGFLGGLRAWNOVLOUGTDROGGGANA AVVITALSTATATAGGSGROOFLGGLRAWNOVLOUGTDROGGGANA CERTSTSTTTAKFETTLANGFGGOGGAFLANGVANTAGGGGGAFLANG AVVITALSTATATAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				GHMTTLSGEEISYTGSDGIEGGLLASIRMNHQALVRKLPDLEKT
GSLĀGAI JOSS IY PMEVLKTRMALRITGOY SOMILOCAREI LARE GVAĀFYKGYVPIMLGI IP YAGIDLAVYETLKNAMLONYAWSAD PGVPULLĀCCTMS STCGOLĀSYPLALVRITMOĀGAS IEGĀPĒVT MSSLFKHILRTEGĀFGLYRGLĀPRĪMKVI PĀVSI STVVVENIKI TLOVOSR APPĀGRRĪMOĀĀPRĀGGGĀLLLKHĪVSSCLCRĀWTĀPĒSTSOKO EPLĪVSCLĒPĪVĀS SSSSI ISGSYPOYĀKI INKRĒGĀGGRSPĒDĪSOKO HYOMLOVPĒGNIKO I SALĀTOGRYSS SDWYTOYRNIK STOKOM HYOMLOVPĒGNIKO I SALĀTOGRYSS SDWYTOYRNIK STOKOM KRYHODGNI WĀPĒNI INSDGVVRHĒLOŅPI I LARYVIS IPVĒMNO EGRIGLRI EVVĢCSVWĀDVI INPŪGIVULPY PRĒMKKMKTI,KDVI ALĀFKTSĒSĒCVI LHGĒGOĢODYITLĒLKĀRĀLVIJENGBŅOL GPI YGGTSVMROSLLODHIHMENVU IERĢGRI JORDSOM, WAS TNOĒPĒVIJLDIYĒ I TĒGGI PPSGKPSSSS KNĒKGCMĒS INTNG WINTDLĀRKKĀLĒPĒNNOMI,SPĒCVĒPYT VĒMĀTSYLĒVĒĢ RLĀNOLĪ FŠVSFOR TRĀMBNOLĪMOSHMENVE ILDITISKVĢ WHI NITOTKMSOLI DI SSOSGLANGOMHEVE PĀRTSYLĒVĒĢ RLĀNOLĪ FŠVSFOR TRĀMBNOLĪMOSHMENVE ILDITISKVĢ WHI NITOTOM BOLD ID ISSOSGLANGOMHEVE PĀRTSYLĒVĒĢ RLĀNOLĪ FŠVSFOR PĀVĀDRĀMS IDMĀCAI IDROVPINCĒ HGĢKCSĢTŪMPŠ KRCTDĒTĒTOSAGĀCUMS IY PSGEAPKHLĀGOT SNYYMI DPOSSCPLĀPĪKVYCANNTĒDKWĀTI VISHDLOMOTPĀVĢ YNPĒKSVĀVOLVYSASMODI SALTDSACĪVĒVĀ YCKMSKLL NTPOSSPTTMVKOKANĒRHYVMGSSGPI OKCĀCGI ERNITOPK YYCHOLĀDĀVĀKMRĀDĀGI PĀSKĀVE STOKOMETOPK YYCHOLĀDVĀNĀMA SALTDSACĀVE STOKOMETOPK YYCHOLĀDĀVĀMS KROĀGI PĀSKAPS PĀRGĀMĀKĀ SVĢPLRCĢGODRINVANAAS FINDESS VLIHEST FOGETSĀDI SPĀFK TLIPMĢVPLENMIKEDĪTI KLĒLKSATĒVSFS PĀGOKĀGĀVE VĀ SPĪPILMDOMHRVTJĀRRNĪVĀSALTVARDOTSSKOLNAPOGONSHĒBLĀQ ELYSOLFVĢGRĀGGOĢGF LGCIRSLĀMRĀVILDLERRAKVTSOFĪ SGCSGRCTSVĀTCENĢGKLERVĀMYSCOLFNAMĢOTELOKĀR VGĀFFĒGOMBRIND FĀRĀTARDSSSRVINAPOGONSHĒBLĀQ EETRFSFSTTRAPCILLĪVI SETTIPLĀLVINĀTSOLOR VĀNIĀG GTREPNI IDVORNAMANGOPRSVNI THREKTI FLKLICHTPSVSY HLPSSSDTLPNSKSLĀFIGĀVI IETKĀLORPI SKORĀ PĀRĀ SAVV-SWILTAASTKVOALILĀDĀLETKĀK PĀGERĢRĀKĀRĀ KPĀRPĀRĀMKĀRĀ SĀRĀVĀNI JOSENVĒNASALĀVĀNI GGGVI AMA NAVVI FTDSLICTĪV VĻVĒ PĀS PĀRBĀKGRĀGĀKĀK KPĀRPĀRMILDBIRSĀRĀPĀ PĀRĀGRĀGĀKĀKĀ KPĀRPĀRĀMĀRĀ SĀRĀVĀ PĀRĀVĀRĀ PĀGRĀGĀRĀKĀ KPĀRPĀRĀMĀ PĀRĀVĀNĀ PĀRĀVĀNĀ PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀRĀVĀNA PĀ				GHK
GVARFYKGYVPRMIGTIPYAGIDLAVYETLKNANLOHYAWNSAD PGVPVILACCTMSSTCGQLASYPIALVRTEMQOASIEGAPEVT MSSLFKHILRTEGAFGLYKGLAPFKKVIPAVGASIEGAPEVT MSSLFKHILRTEGAFGLYKGLAPFKKVIPAVGISTYVVVENIKI TLEVOGR 4PPGGRRMQAAPRAGCGAALLLMIVSSCLCRAWTAFSTSQKCD EPLVSGLPPVAFSSSSISGSYSFYAKINKRGGAGGKSFDSDS HYOMLQVDFGNKGIGSALATGGRYSSSDVYBMINFDGRNM KPYHODGNIWAFPGNINSDCVVRHELOPPIIARYVRIVPLDWNG EGRIGLRIEVYGCSYWADVINFDGHVVLPYRFYRKKMKTLKDVI ALMFKTSESECVILHCEGGCOCHYTTELKKALVLSINLGSNQL GPIYGHTSVMTGSLLDDHWHSVVIERQGRSINLTDESWOFFR TNGEFPYLLDLYPSITFREMYGGLLDYFFRARIKKALLSINLGSNQL GPIYGHTSVMTGSLLDDHWHSVVIERQGRSINLTDESWOFFR TNGEFPYLDLDYFITFGEFPFFAPHICHVENIVTENUTENUTENUTENUTENUTENUTENUTENUTENUTENU	6789	2	678	GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA
PGVPVILIACGTRESTCGOLASYPLALUFTRMAQAS LEGAPEVT MSSLFKHILRTEGAFGLYRGLAPNFMKVI PAVSISYVVYENLKI TLEVQSR APPAGRRMQAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD PELVSCLPPVAPSSSSSISSGSYSGYAKIKRGGAGGMSPSDSD HYOMLQVDFGNEKOJ SALATOGRYSSSDWVTOYBMI. YSDTQRNM KPYHQDGNI WAPPGNI NSDCVVRHELQHP I LRYVRI VPLDWNG EGRIGLRI EVVGCSYWADVINFDCHVVLPYR FRKKMKTLKOVI ALMFKTSESECVI LHCEGQOGDYTTLELKKAKLULSINLGSNQL GPI YGHTS WITGSLLDHMBHSVVI TERGGIS HIVTLDGSNQMFR TNGEPDYLDLDYEI TFGGI PPSGR PSSSSRNYRGCMES INYNG WNI TDLARRKKLEPSNVGNLSFSCVEPYT VPV FNATSY LEVGG RLNOLFSVSFORT WNNPRGLLVFSHFADRIGNVEIDLTESKVG VHINI TOTKMSOI DI SSGSGLMDGOWHEVRI-LAKENFALLTIDG DEASAWRTHSPLOU KYTGEKY FFGGFI LOMONSISSIVLOPS FGGC MOLI OVDDOLVNI, YEVQRKFGSFANVSI DMCAI I DRCVPNICE HGGKCSOTTMOSFSCKCTGFT WNNPRGLLVFSHFADRIGNVEIDLTESKVG VHINI TOTKMSOI DI SSGSGLMDGOWHEVRI-LAKENFALLTIDG DEASAWRTHSPLOU KYTGEKY FFGGFI LOMONSISSIVLOPS FGGC MOLI OVDDOLVNI, YEVQRKFGSFANVSI DMCAI I DRCVPNICE HGGKCSOTTMOSFSCKCTGVST FTGGT SGATCHRIS SSIVLOPS FGGC MOLI OVDDOLVNI, YEVQRKFGSFANVSI DMCAI I LORCYPNICE HGGKCSOTTMOSFSCKCTGVST FTGGT SGATCHRIS FRUSCHAFT SNYWID PDGSGPLGPLKVYCNWTEDKVT VSHDLOMOTPVUG YNPEXYS YTOLVYSASHDOJ ISAITOSAEVCCO YVTY CKMSELL NTPOSSPY THWOKANEKHY YWGGSGEG I OKCAGGI ERNCTOPK YCNCDADYKOWRROBGFILSY KOMLEVSOVVCOTTOR GSEAKL SVGPLRCOGDRNWANAS FRIPSSY LHEFTGGSTSADI SFYKL SVGPLRCOGDRNWANAS FRIPSSY LHEFTGGSTSADI SFYKL SVGPLRCOGDRNWANAS FRIPSSY LHEFTGGSTSADI SFYKL SVGPLRCOGDRNWANAS FRIPSSY LHEFTGGSTSADI SFYKL SVGPLRCOGDRNWANAS FRIPSSY LHEFTGGSTSADI SFYKL SVGPLRCOGDRNWANAS FRIPSSY LHEFTGGSTSADI SFYKL SVGPLRCOGDRNWANAS FRIPSSY LHEFTGSTSADI SFYLL SVGPLRCOGDRNWANAS FROM STRONGTOR FRAPTEGHTRI ELYSLFVGGGGGOGOFILGCT RIJRINGVTLDLEERA KVTSGFI SGCSGRCTSYGTNCENGCKLERYHGYSCCCSNTAYDGFTCKXG VGFRFSSNTNNDPTSCRRPTTARDSSSCRVDAPPOONSHPLAQ EETRSFSTTAPCILLYTSSFTDELAVLVXPOSCLOT RYNLOK GTREPYNI DVHRWARAMOOPHSWNI TRHEKT I FIKLDHY PSWS HLPSSSDTLFNSKYSLFIGKVI ETGGI DQEI HKYNTPGFTGLS RVOFNOJAPHTONGTAPA TRANGTROGYLAMG SAVV-SWLTAASTKVOATILLOPLE ILGIOI TAFNALSATHENO NSGI I ESSVETTININ FTOMPAGRCA PAWGY FFTSFMKHEDV EEYVYLHHINGNTVF				GSLAGAIAOSSIYPMEVLKTRMALRKTGOYSGMLDCARRILARE
MSSLPHILLRTEGAFGLYRGLAPNFMKVI PAVSISYVYENLKI TLGVQSR APPAGRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD EPLVSGLPHVAFSSSSISGSYSFGYAKINKRGGAGGWSFDSDS HYWALGVDFGRKGISALNGGRYSSDSDY HYWALGVDFGRKGISALNGGRYSSDSDY HYWALGVDFGRKGISALNGGRYSSDSDY KPHODGNIWAPFGN INSDGVVRHELQHPILARVYRIVEDLDWIG EGGIGLRIEVGCYWADVINFDCHVULPYRMIKYSDTGRNW KPHODGNIWAPFGN INSDGVVRHELQHPILARVYRIVEDLDWIG EGGIGLRIEVGCYWADVINFDCHVULPYRMIKYSTUPLDWIG GPIYGHTSWMTGSLLDDHHMHSVVIERGGRSINLTDLBSWQHFR TNGEPFYLLDLYFITTGGIPPSGKPGSSSRNFKGCMESINYNG VNITDLARRKKLEPSNVGRLSFSCVEPYTVPVFFNATSYLEVPG RLANCDLFSVSFOFFTNIWRGLLVSHIFANCWEIDLTSKVE WHINITOTKMSOIDISSGGLMDGWHEWRFLAKENPAILTIDG DEASAVRTNSPLQVKTGEKYFFGGFLNOMNNSHSVLOPSFOCC MQLIOVDDDLWLYEVAGRKFGSFANVSIDKGAIIDRCVPINCE HGGKCSQTMDSFKCTCDETGYSGATCHNSIVERYPHALIFING SNYWHIDPDSSCPLGFLKVVCNAMTEDKWYTCHMELDKYTFVKGMELL NTPDGSPTYTWWGKANREHYVGMSGGSJGKACGGISRNCTDFK YYCNCDADYKOWRKDAGFLSYKDHLDVSOVVGDTDROGSEAKL SVEPLRCOGDRNIWNAASFPRPSSYLHFSTFOGSTSALISFYFK SUPPLRCOGDRNIWNAASFPRPSSYLHFSTFOGSTSALISFYFK SUPPLRCOGDRNIWNAASFPRPSSYLHFSTFOGSTSALISFYFK STPLINDDOWHRVTAERNVKOASLOVDRLPQOIRKAPTEGHTRL ELYSOLFVGGAGGOGOFLCITRISRNGWTDLEERAKVTSGFI SGCSGCTSYGTNCENGGKCLERVHGYSCDCSNWTADGTPCNKU VGAFFBEGMWRLWR PAPATTARDSSSRVDAPDOONSHEDLAQ EEIRFSFSTTKAPCILLYISSFTDPLAVLVKPTGSLOIRNILG GTREFYNIDVDHRRWANAGGPHSVNITRHEKTIFLKLHPYBVSY HLDSSSDTLFNSFNSLEJGEKVIETGKINDCHHKVTTPGFTGCLS RVOFNOIAPLKAALROTNASAHVHIGGELVSSNCGASPLTLSPM SATOWHLIGHLBASAGDFPNNGOGSPTRKVARNSAIIGGVI A\VVIFTPSLCTPVUP-SR-HKYBFHGTLFIPMEAAGGSRQK KPGRRPSMNNDPPTSGRPIDESKKEWPHLRAGGLAWG NSGIIFSSVETNIONFFDWMGRGABVSGVFFTFSMKHEDV EEVYVILMHNGRTUPSMYSYEMKGKDTSSNHAVLKLAKGDEVW LRMGNGALHGDHORFSTPAGFLIFFTK 792 33 1073 VRITNAGDWDHTSLASSESPKGAGHIVSTEKTILAVERNKVLL PPLWNRTFSNGFDDFSCCLGSYGSDRVLMTFENLARHEGISA 1TISDVSGTIVSAGGADHSLMWNWQPLASITTAMGGCLCAV CPSPTTIUTTSGTSTVCVWELSMYKGREGRERLRQALYGHTOAV TCLAASVTFSLUNGSGODCTCLLUDLJHLTHVTRLPAHREGISA 1TISDVSGTIVSAGGAHLSLMWNVQPLASITTAMGFGCATCC CLMEGRANDTSOITIIGSSDCMWRVWKYVCCEDVCSWTASSRR				GVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSAD
TLGVGER APPÄGRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD EPLVSGLPHVAFSSSSSISGSYSPGYAKINKRGGAGMSPSDSD HYOWLQVDPGNKKQISAIATOGRYSSDWTOTYMM,YSDTGRNM KPHYHOGANIMAPPGNINSDGVWHELQHPIIARYVSILVPLDWNG EGRIGLRIEVYGCSYWADDVINPDGHVU,PYRFRKKMKTLKDVII ALNFKTSESEGVILHGEGQOGDYITLELKKAKLVLSINLGSNQL GPIYGHTSWMTGSLLDDHHHHSVVILENGGRSINLTLDRSMQHFR TNGEFPYLDLDVEITFGGIPFSGKPSSSRRNFGCMSINYND WINITDIARRKLEPPNGNINSPSCUEPYTVPVFPNATSYLEVPG RLNODLFSVSFOFRTWNPNGLLVFSHFADNLGNVEIDLTESKVG WINITOTKMSOIDISGSGLNDGOWHEVFLAKEMFAILTIDG DEASAVRTNSPLQVKTGEKYFFGGFLNGMINNSSHSVLOPSFQGC MOLIOVDDQLVMLYEVAQRKPGSFANVSIDNCAIDICVPHHLG HGGKCSOFTMDSFKCTCSTCTYSGGATCHISIYEPSCEAYKHLGOT SNYYWIDPDGSCPLGPLKVYCMNTEDKWRTIVEPSCEAYKHLGOT SNYYWIDPDGSCPLGPLKVYCMNTEDKWRTIVEPSCEAYKHLGOT SNYYWIDPDGSCPLGPLKVYCMNTEDKWRTIVEPSCEAYKHLGOT SNYYWIDPDGSCPLGPLKVYCMNTEDKWRTIVEPSCEAYKHLGOT SNYYWIDPDGSCPLGPLKVYCMNTEDKWRTIVEPSCEAYKHLGOT SNYYWIDPDGSCPLGPLKVYCMNTEDKWRTIVEPSCEATYKHLGOT SNYYWIDPDGSCPLGPLKVYCMNTEDKWRTIVEPSCEATYKHLGOT SNYYWIDPDGSCPLGPLKVYCMNTEDKWRTIVEPSCEOTYSYSTKGMSLL NTPDGSPYTWWGRANEKHYYWGSGGFOIKKCACGIERNCTIPK YYCNCDADYKOMRNDAGFLSYKHHSTFOGETSADISFYFK TLTPWGYFLENMGKEDFIKLELKSATEVSFSFDUGGPVELVVR SPPTLMDDDWHHRUTAERNWKOASLOVDELPOQIRKAPTEGHTAL ELYSOLFVGGAGGQOGFLGCIRSLRMNGVTLDLEERAKVTSGFI SGCSGCTSYGTNCENGGKCLERYNGYSCDCSNTADGETFCNKD VGAFFEEGGMULRYNFGAPATNARDSSSKVDNAPDQNONSHPDLAO EEIRFSFSTTKAPCILLYISSTTDFLAVLVKPTGSLQIRYNGFLAN GTREPNYIDDVDHRWNANGOPSVNITHETIFLIFLLINDFYBUGHTPCKLS RVOFNOIBPLKAALROTNASAHVHIQGELVESKOGSBPLING FERNANDIDPTSGARARONDPTSGOANNOPNSAIIGGVI A\VVIFTSBLCTPV\UP*SR*HVSPHKGTLPIPDEKGAGSRQK KPGRPESHNDDPTSGARARONDPTSGOANNOPNSAIIGGVI A\VVIFTSBLCTPV\UP*SR*HVSPHKGTLPIPDEKGAGSRQK KPGRPESHNDDPTSGARARONDPTSGARDFOGNYFFTSSMKHEDDV EEVYVLHMINGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW LRNGNCALAGGODOANSTROLFICKYWELSMTKGRRGREGLRLROALVSULT PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFEHAARGGCLAAN CESPTTIVTSGTSTVCVWELSMTKGRRGREGLRLROALVSULTONAV TCLAASVTFSLLVSGSODCTCILMDLOHLTHVTRLPAHREGISA 1TISDVSGTIVSCGGABLSLIMNVNOQPLASITTAWGPEGAITCC CLMEGFRANDTSQIITGCSGARAUNCOPLASITTAWGPEGAIT				PGVFVLLACGTMSSTCGQLASYPLALVRTRMOAOASIEGAPEVT
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EEIRFSFTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLG GTREPYNIDVDHRNMANGQPHSVNITRHEKTIFLKLDHYPSVSY HLPSSSDTLFNSPKSLFLGKVIETGKIDQEIHKYNTPGFTGCLS RVQFNQIAPLKAALRQTMASAHVHIQGELVESNCGASPLTLSPM SSATDPWHLDHLDSASADFPYNPGQGQAIRNGVNRNSAIIGGVI A\VVIFTPSLCTP\VLP*SR*HVSPHKGTLPIPNEAKGAGSRQK KPGRRPSMNNDPPTSQRPIDESKKEWPHLRGGYLAMG 6791 1801 1193 TGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPEL/PGW SAVV*SWLTAASTKVQAILLPQPLE*LGLQIAFMASLATHFSNQ NSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDV EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW LRMGNGALHGDHQRFSTFAGFLLFETK 6792 33 1073 VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVLL PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV TCLAASVTFSLLVSGSQDCTCILWDLDHLTHTVRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG			İ	
GTREPYNIDVDHRNMANGOPHSVNITRHEKTIFLKLDHYPSVSY HLPSSSDTLFNSPKSLFLGKVIETGKIDQEIHKYNTPGFTGCLS RVOFNOIAPLKAALROTNASAHVHIQGELVESNCGASPLTLSPM SSATDPWHLDHLDSASADFPYNPGQGQAIRNGVRNSAIIGGVI A\VVIFTPSLCTP\VLP*SR*HVSPHKGTLPIPNEAKGAGSRQK KPGRRPSMNNDPPTSQRPIDESKKEWPHLRGGYLAMG 6791 1801 1193 TGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPEL/PGW SAVV*SWLTAASTKVQAILLPQPLE*LGLOIAFMASLATHFSNQ NSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDV EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW LRMGNGALHGDHQRFSTFAGFLLFETK 6792 33 1073 VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVLL PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG				
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NSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDV EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW LRMGNGALHGDHQRFSTFAGFLLFETK 6792 33 1073 VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVLL PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG	0,91	1001	1133	· · · · · · · · · · · · · · · · · · ·
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6792 33 1073 VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVLL PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG				
PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG	(200	<u> </u>		
CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG	6197	33	1073	
TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA 1T1SDVSGTIVSCAGAHLSLWNVNGQPLAS1TTAWGPEGAITCC CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG				
ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG				
CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG				15
	ļ			ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC
APGSASKPKRPOVGEEPGI.ESRAGR*HCFDREAOONOP\PVTAL	i			CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG
1 Seriett and Kroppi appointment to the first training				APGSASKPKRPQVGEEPGLESRAGR*HCFDREAQQNQP\PVTAL
AVSRNHTKLLVGDERGRIFCWSADG*EERGSRGSGTTVPG	}	_		AVSRNHTKLLVGDERGRIFCWSADG*EERGSRGSGTTVPG

	I becali	Precicted end	Amino acid segment containing signal peptice
SEO	Predicted beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID		1	
NO:	nucleotia	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	K=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amine acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stcp
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
Í	sequence	1	\=possible nucleotide insertion)
6793	2340	805	GRKEANY\YGSLTCAGTVSLGLDAEGOEVFVPFSAVLPMVAFND
	1		LVFDGWDISSLNLAEAMRRAKVLDWGLQEQLWPHMEALRPRPSV
		1	YIPEFIAANOSARADNLIPGSRAOOLEOIRRDIRDFRSSAGLDK
	ì	1	VIVLWTANTERFCEVIPGLNDTAENLLRTIELGLEVSPSTLFAV
	}		· · · · · · · · · · · · · · · · · · ·
	1		ASILEGCAFLNGSPONTLVPGALELAWOHRVFVGGDDFKSGOTK
			VKSVLVDFLIGSGLKTMSIVSYNHLGNNDGENLSAPLCFRSKEV
			SKSNVVDDMVQSNPVLYTPGEEPDHCVVIKYVPYVGDSKRALDE
	i	1	YTSELMLGGTNTLVLHNTCEDSLLAAPIMLDLALLTELCORVSF
		1	CTDMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI
{			ENILRACVGLPPONHMLLEHKMERPGPSLKRVGPVAA:TYPMLNK
			KGPVPAATNGCTGDANGHLQEEPPMPTT*GPGHTVSRLFLPAAP
1	1		HDPTLKAPTNKGRCHFSPPSTWGSWGL
6794	1.69	1349	DDVKRKPEASAH*EKPGPPSRPGVRGGRERAGGRGSHGARSCR\
1	1		EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGEKTYTCRCRLFVG
1		1	NLPTDITEEDFKRLFERYGEPSEVFINRDRGFGFIRLESRTLAE
1			IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELLEQA
	ļ.		FSOFGPVEKAVVVVDDRGRATGKGFVEFAAKPPARKALERCGDG
ĺ			1 -
			AFLLTTTPRPVIVEPMEQFDDEDGLPEKLMQKTQQYEKEREQPP
1		1	RFAQPGTFEFEYASRWKALDEMEKQQREQVDRNIREAKEKLEAE
1			MEAARHEHQLMLMRQDLMRRQEELRRLEELRNQELQKKKQIQLR
	1		HEEEHRREEEMIRHREQEELRRQQEGFKPNYMENYVCHFLR
6795	1740	1010	GPRRQTQVRDHELDSF*DWAAQETDCAQNSGERL*KGV/LENFS
		ļ	TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNC
1		1	EKVNQIQKTVIEPLKKFGSVFPSLNMAVKRREQALQDYRRLQAK
Ì	İ		VEKYEEKEKTGPVLAKLHQAREELRPVREDFEAKNROLLEEMPR
			FYGSRLDYFOPSFESLIRAQVVYYSEMHKIFGDLSHOLDQPGHS
	Į.		DEGRERENEAKLSELRALSIVADD
6796	48	683	GKEIQIPTIKLANLLFGLE*PVGALGKGVVSF**SHVALGQLGW
l			LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSFVGACPSLNPPET
l			SVCEGRDCWQR*LPRLFSALVGQPGCWPQGAPPERCV*PGRCKW
1		1	HLOSOVLR*ERRRCCRCLPRFA*GWRRRHORLGLGIHPAPLGST
İ	1	1.	SPPHPEGNSCOCRR*GWAAELRLPSSVVL*GKLGC*
6797	1620	211	TERMTPSOPTRGSSCTRPSSMLWTSTWRCLTCHWAGMEMSVVGV
0131	1620	211	TLGPMAQGLLSASGTTTEATWTRPTTHLTLIRWWLLTASRVDPF
1		1	ERPPPPPSDDLTLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP
	ì	1	LTSRASSIMRSRTAIPSAS*SRLTTKHTVGGSPSAWRPRPTSRS
1			VSTPVSSSTETTASGSCLTWWSSSPAPCPSSSAPAHSFEASCCK
1			TSLWGSCGGSGDGSSACGSGWNLSMAGTSCSSPAMCSFSRAPS*
		1	RSASRPRTWRATTSAASSWAPRRCWCGWA*SAT*PSSTTTISSS
1			PHCGWPCPASCASAAAWLSSTWATASVAGSCWGPIM*SSAHSPW
l			CLSACSRSSMGTTCL*RSPP\SGASRAAAAWCGSSPSSTFTPSS
[Į.	ASSSTWCSASSSRSSPAPTTPSSIPAAQAQRRASCRPTSHSART
			APPPASSAAGAARPAAFSAAAEGTPRRSIRCW
6798	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
1	3033	1	ALWGOLRGSGLGRGTTMAKEGOPGSPRLSALECVLLVPO\PQIA
1	1	İ	VRULAHKIOSPOEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
1		i	
	1		ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
			VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
			TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
1			ENKRRTLFKLASETEDNONSLGDILQASDNLSRVINSYKTIIEG
			QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
į			PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
1		1	SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
1	1	1	PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
	!		APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHFLDAL
1			DOLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
			- POSSESSAN A POSSESAN DE LA POSSESA DE LA P

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amine acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
{	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
 		 	PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
	1		RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
}	1		MKVKLOPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
			LTFALGEQLSTEVGEVDQFPPVEQWGNL
6799	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
1		1	ALWGOLRGSGLGRGTTMAKEGOPGSPRLSALECVLLVPQ\POIA
1		1	VRLLAHKIQSPOEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
l		1	ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
			VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
		ļ	TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
1			ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
			QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
]			PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
1			SWLDEELLCLGLADPAPNVPPKESAGNSOWHLLOREOSDLDFFS
		1	PRPGTAACGASDAPLLOPSAPSSSSSQAPLPPPFPAPVVPASVP
			APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
l	ł		DOLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
		ļ	PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
			MKVKLOPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
1			LTFALGEQLSTEVGEVDOFPPVEQWGNL
6800	404	1646	RRSPSTGLSPVPCPSSPSLSDYSIPWSLLLSGTIAWATPGK*AG
			*PQAW*LGLAPAIAFI/GLTRGRKQNKEKMAEGGSGDVDDAGDC
			SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARARA
l			RATRARRAVOKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILE
ļ	1		AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL
i			IVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLL
			TMMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNLAE
ļ			NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN
			FKWEENEPTQNOFGEGSLFFFLKEFQVCADKVLGIESHHDFLVK
}		ļ	VKVGKFMAKLAEHMFPKSQE
6801		1755	SAEEFESQQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVERL
}			YAASDMLQLEYVREACASFLARRLDLTNCTAILKFADAFGHRKL
[1	1	RSQAQSYIAQNFKQLSHMGSIREETLADLTLAQLLAVLRLDSLD
(VESEQTVCHVAVQWLEAAPKERGPSAAEVFKCVRWMHFTEEDQD
		1	YLEGILTKPIVKKYCLDVIEGALQMRYGDLLYKSLVPVPNSSSS
1			/R*QQQLSCICSRKSTPETGYVCQGDGDLLWTPQRSLS\RYDPY
	1	1	SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDIYLAAQPRKDLW
1			VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPITGVK
1			LKEVECYSVQRNQWALVAPVPHSFYSFELIVVQNYLYAVNSKRM
			LCYDPSHNMWLNCASLKRSDFQEACVFNDEIYCICDIPVMKVYN
]		1	PARGEWRRISNIPLDSETHNYQIVNHDQKLLLITSTTPQWKKNR
j			VTVYEYDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLEPG
		1	OSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVQ
1			VAPORNAQDQQGSL
6802	1.57	1341	ETFPLFFFLLSKTPGKTASMAHFVQGTSRMIAAESSTEHKECAE
1		1	PSTRKNLMNSLEQKIRCLEKQRKELLEVNQQWDQQFRSMKELYE
1		1	RKVAELKTKLDAAERFLSTREKDPHQRQRKDDRQREDDRQRDLT
Ī			RDRLQREEKEKERLNEELHELKEENKLLKGKNTLANKEKEHYEC
1	1		EIKRLNKALQDALNIKCSFSEDCLRKSRVEFCHEEMRTEMEVLK
ĺ			QQVQIYEEDFKKERSDRERLNQEKEELQQINETSQSQLNRLNSQ
1			1KACOMEKEKLEKOLKOMYCPPCNCGLVFHLODPWVPTGPGAVQ
[1	KOREHPPDYOWYALDOLPPDVOHKAN/DWCLAPPPVCCQAG/PR
		}	TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRER
ļ		}	G
6803	2	2203	KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQQFYLALDN
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nuclectide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotia:	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	b=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acic	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acić	sequence	Codon, /=possible nucleotide deletion,
	seguence		\=possible nucleotide insertion)
1			KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSMLDEDGTSLNS
j		}	SILAALRKMODGYFGGARVQTGKLSEFLTTSCCTHLSFMDPGPE
Ì	1		GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDEVARYLDHLL
į			AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLVTKAKELHVQ
1	1	İ	NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD
			OSGEVDFKALVLOLKETSSLQEQADILYMLYTMKGPDWNTELYN
l	ł	1	ERSATVRELLTELYGKVGEIRHWGLIRYISGILRKKVEALDEAC
	1	}	TDLLSHOKHLTVGLPPEPREKTISAPLPYEALTQLIDEASEGDM
ļ.	1	ì	SISILTQEIMVYLAMYMRTQPGLFAEMFRLRIGLIIQVMATELA
1		Į.	HSLRCSAEEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR
1		1	PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEIKQVEFRRLS
-	[1SAESQSPGTSMTPSSGSFPSAYDQQSSKDSRQGQWQRRRRLDG
1	1		ALNRVPVGFYQKVWKVLQKCHGLSVEGFVLPSSTTREMTPGEIK
1	1	1	FSVHVES\VLNVLLRPEYRQLLVEAILVLTMLADIEIHSIGSII
1		1	AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD
			SAPSGRFGTMTYLS\RAA\ATYVQEFLP\HSICAMQ
6804	1	951	GSPGKKEEKAKNKESLCMENSSNSSSDEDEEETKAKMTPTKKYN
İ	}		GLEEKRKSLRTTGFYSGFSEVAEKRIKLLNNSDERLQNSRAKDR
l .			KDVWSSIQGOWPKKTLKELFSDSDTEAAASPPHPAPEEGVAEES
ì			LQTVAEEESCSPSVELEKPPPVNVDSKPIEEKTVEVNDRKAEFP
t			SSGSNFSA*IPLPYLHLNRLHQSL*QKGSRQOSSVTVSEPLAPN
1			QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF*CQCEL
}	1	1	KQ**SARTRTS*KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK
L			OOKEGKRHK
6805	1539	206	RQPDLKYFGKSFDVSVSESSSLLSNDLPKFADGI KARNRNQNYL
			VPSPVLR1LDHTAFSTEKSADIV1CDEECDSPESVNQQTQEESP
ł		i	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA
i		1	KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS
			DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDFYI
1	!		CKYCDYKTV1FENLSQH1ADTHFSDHLYWCEQCDVQFSSSSELY
1			LHFQEHSCDEQYLCOFCEHETNDFEDLHSHVVNEHACKLIELSD
i		1	KYNNGEHGQYSLLSKITFDKCKNFFVCOVCGFRSRLHTNVNRHV
1	1		AIEHTKIFPHVCDDCGKGFSSMLE\1AKHLNSHLSEGIYLCQYW
	1		FYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP
			VHETT
6806	272	3794	VALCEPNSDPVMFMDAFYGCLLAELGPVP1EVPLTRKDAGSQQV
1	1	1	GFLLGSCGVFLALTTDACQXGLPKAQTGEVAAFKGWPPLSWLVI
1			DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA
1	1	ł	SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLNHGVLTSVMNR
1			MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ
1]	J	RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV
1		1	1CPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD
1		1	TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV
1		1	SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG
1		1	FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY
1		1	RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID
		Į.	SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN
1]	Į.	VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR
	I	1	ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT
1	1		I CONTROL THE SECUENCE OF CUCCINALIVED CONTROL TAN
			STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA
			FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT
			FYGCLYCGCVPVTVRPPHPONLGTTLPTVKMIVEVSKSACVLTT OAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP
			FYGCLYCGCVPVTVRPPHPONLGTTLPTVKMIVEVSKSACVLTT OAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ
			FYGCLYCGCVPVTVRPPHPONLGTTLPTVKMIVEVSKSACVLTT OAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ IAICLDPYCGLGFALWCLCSVYSGHQSVLVPPLELESNVSLWLS
			FYGCLYCGCVPVTVRPPHPONLGTTLPTVKMIVEVSKSACVLTT OAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ

			·
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
: ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1 10:	nucleotide	location.	Glutamic Acid, F=Phenylalanine, G=Glycine,
; •	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	!	\=possible nucleotide insertion)
			LOGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKIL
			PGVKVIIAHTETKGPLGDSHLGEIWVSSPHNATGYYTVYGEEAL
ł			HADHFSARLSFGDTQTIWARTGYLGFLRRTELTDASGGRHDALY
			VVGSLDETLELRGMRYHPIDIETSVIRAHRSIAECAVFTWTNLL
		1	VVVVELDGLEODALDLVALVTNVVLEEHYLVVGVVVIVDPGVIP
	ļ	}	INSRGEKORMHLRDGFLADOLDPIYVAYNM
6807	1444	606	VGHDTVHAMFTCFPKCLGFSPPVNVTVSPRSEESHTTTVSGGNG
			SVFQAGPQLQALANLEARRGS1GAALSSRDVSGLPVYAQSGEPR
{		İ	RLTQAQVAAFPGENALEHSSDQDTWDSLRSPGFCSPLSSGGGAE
		· ·	SLPPGGPGHAEAGHLGKVCDFHLNHOOPSPTSVLPTEVAAPPLE
İ			KILSVDSVAVDCAYRTVPKPGPOPGPHGSLLTEGCLRSLSGDLN
			RFPCGMEVHSGORELESVVAVGEAMA\LKFPMGAMSYCLRDRSR
}	1		FLFRLPMGLSCPLOVO
	2063	725	
6808	2063	737	GVGSGAASALARSRPLASRLSSRRRTRAPRSGAMORIAMDLRML
		1	SRELSLYLEHOVRVGFFGSGVGLSLILGFSVAYAFYYLSSIAKK
ł		i	PQLVTGGESFSRFLQDHCPVVTETYYPTVWCWEGRGQTLLRPF\
Ì			ITSKPPVQYRNELIKTADGGQ1SLDWFDNDNSTCYMDASTRPTI
1			LLLPGLTGTSKESYILHMIHLSEELGYRCVVFNNRGVAGENLLT
1		1	PRTYCCANTEDLETVIHIVHSLYPSAPFLAAGVSMGGMLLLNYL
		i	GKIGSKTPLMAAATFSVGWNTFACSESLEKPLNWLLFNYYLTTC
ļ		Į.	LOSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYQTI
ŀ			DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHAIPIETAKQN
	1		PNVALVLTSYGGH1GFLEG1WPRQSTYMDRVFKQFVQAMVEHGH
		<u>] </u>	ELS
6809	939	65	DYSGQTPVPTEHGMTLYTPAOTHPEQPGSEASTQPIAGTQTVPQ
i			TDENAQTDSOPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF
			GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
			EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
			VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPPIPTYG
	1		AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP
L			TRT1TPSGPRRPTALEPCETFHRFLLGP
6810	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
1	1	1	TDEAAQTDSQPLHPSDPTEKQQFKRLHVSNIPFRFRDPDLRQMF
1	!	İ	GQFGKILDVEI1FNERGSKGFGFVTFETSSDADRAREKLNGTIV
			EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
			VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG
1			AVVYQDGFYGAEI\LEATQPTDTLSPLCRRQPTATVTAESTQLP
		1	TRTITPSGPRRPTALEPCETFHRFLLGP
6811	1522	65€	DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME
			FSGSDEDFODLLHFGRDRADSTOCRLSRRNSTDSRPVSVTYRFG
!		i	SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN
!	ļ	1	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV
İ	Ì		SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK
1	!	1	TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI
}			VTACQEGFICTWGRPGKVVSFNP
6812	4001	1682	EDAVFSLDLSTI1QGTWPLNGEELKSNEFEGQVEPGALRYRIEQ
ì			KGLOHRLILHAVKHODSGALVGFSCPGVQDSAALTIQESPVHIL
1			SPODKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL
	ļ	1	VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV
ł	İ		HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE
			ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI
1			TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE
	1	1	EVVESPALLLOKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT
\	1		VTVTEPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK
ĺ			DGLEVEESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA
1			FFTVTVTEPPVQFLALETTPSPLCVAPGEPVVLSCELSRAGAPV
	4	1	LEININIERANGE PUPETING SEPCANGES AND CETQUAREA

SEC	Predicted	Predicted end	Amino acid segment containing signal peptice
ID	beginning	nucleotic	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location.	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to firs:	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue o:	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acić	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
	 		VWSHNGRPVQEGEGLELHAEGPREVLCIQAAGPAHAGLYTCQSG
1		 	AAPGAPSLSFTVQVAEPPVRVVAPEAAQTRVRSTPGGDLELVVE
į		[LSGPGGPVRWYKDGERLASOGRVOLEOAGAROVLRVOGARSGDA
1			GEYLCDAPODSRIFLVSVEEPLLVKLVSDLTPLTVHEGDDATFR
		į	CEVSPPDADVTWLRNGAVVTPGPCROSCCSYGGCRMCGORKART
1		<u> </u>	CVSKWRQAEWVQRGPCAGCEVGSPCPTTLACPWPRMGTSTASSS
İ	i		MVSYWPTRAPTAARATTIAPWPGSA
6813	9	83€	STOORPGVPAGPRPLDGYLGVADHKPLKMHCRDCALVTSSGHL
1 0013			LHSRQGSQIDQTECVIRMNDAPTRGYGRDVGNRTSLRVIAHSSI
)	1	J	ORILANAHDLLNVSOGTVFIFWGPSSYMRADGKGOVYNNLHLLS
	1		OVLPRLKAFMITRHKMLOFDELFKQETGQ\NRKISNTWLSTGWF
}	!)	TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYYEPFGPDEC
1	1		TMYLSHERGRKGSHHRFITEKRVFKNWARTFN1HFFOPDWKPES
j		ļ	LAINHPENKPVF
6814	3	737	KFRRQEAN/ARERNRMHGLNDALDNLRKVVPCYSKTQKLSKIET
10317	,	1	LRLAKNYIWALSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG
			CLQLNARSFLMGOGGEAAHHTRSPYSTFYPPYHSPELTTPPGHG
		}	TLDNSKSMKPYNYCSAYESFYESTSPECASPOFEGPLSPPPINY
1		İ	NGIFSLKQEETLDYGKNYNYGMHYCAVPPRGPLGQGAMFRLPTD
]	j	ì	SHFPYDLHLRSQSLTMQDELNAVFHN
6815	906	552	OGLDPASQTKVVELLKDGSGRRGDERSSRDMAGGAGPRSESDLE
) 0015	200) 33.	DVGPTAEWNGDGSGSLRRSGSFGKLRDALRRSSEMLVKKLQGGT
			POEPPNPRMKRASSLNFLNKSVEEPTOPGG
6816	1	803	NLLKTHKF\LLGODEDSLHSVPVAOMGNYQEYLKTLASPLREID
	i	1	PDQPKRLHTFGNPFKQDKKGMMI DEADEFVAGPQNKVKRPGEPN
}	•		SPMSSKRRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN
	•	ł	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM
j	į)	TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS
1		1	VDDQKDPVASTLGAMPNTLQITPAMAOGINADIKHQLMKEVRKF
ļ	}	}	GRSK
6817	172	3457	LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS
1		}	DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL
1		1	NNLISPDLEECHTPHKPOKRKSLESSYKDSLLLANSKKTRNYIA
į)	1	IDGGKVLNSKHNGEVYDETSSNLFDSSGQQNPIRTADSLERNEI
	.]	1	LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC
1	1	1	TSFPOALCVOWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE
		1	ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET
1	}	1	CLNEVRDEIFISLOPOLRCTLGDMESPVFAFPLLLKLETHIEKL
İ		1	FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNV1PEWHPLNAAHF
1	1	1	GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF
1		1	EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH
		1	KKFEVPASEIFIVIWERKISQVTDKEAACLPLKKTNDQHALSNE
			KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD
1	1	1	HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV
		1	AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ
1		1	VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ
			LKQFLTPKTEOLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ
]		j	SLKENOKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLOPS
		1	VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP
		ļ	SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH
1			EDLVEGOIHKLRLKLRKKLKAEKKKLAALMSSPOSRTVRSENLE
}	}	i	OVPODGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS
1		1	OTHEEILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS
			EFNDVSQNTHLRQDHNYCSPTKKNFCEVQPDSLTNNACVRTLNL
	1		ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY
6818	2	240	RGFDKVLWT/LSGAVK\CVQFSRISPDGEEGYPGELKVWVTYTL
1			

			·
SEC	Predicted	Fredicted end	Amino acid segment containing signal peptide
10	beginning	nuclectide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location.	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	l to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threcnine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ŀ	seguence	-	\=possible nucleotide insertion)
			DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPO1
6819	1	. 961	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAY
		;	GEEKKKKCNPYVKTYLLPDRSSQGKRKTGVQRNTVDPTFQETLK
1	4	ĺ	YQVAPAQLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS
			TTQSFRWHPLRAKADKYEDSVPQSNGELTVRAKLVLPSRPRKLQ
1			EAQEGTDOPSLHGQLCLVVLGAKWLPVRPDGTLNSFVKGCLTLP
ì	[ł	
j	1	1	DQQKLRLKSPVLRKQACPQWKHSFVFSGVTPAQLRQSSLELTVW
			DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWOKVLSS
6820		ļ	PNLWTDMTLVLH
0620	1014	340	GDMVYIVGHVPPGFFEXTQNKAWFREGFNEKYLKVVRKHHRVIA
		1	GOFFGHEHTDSFRMLYDDAGVPISAMFITPGVTPWKTTLPGVVN
1	l	[GANNPAIRVFEYDRATLSLKDMVTYFMNLSQANAQGTPRWELEY
1		į	QLTEAYGVPDASAHSMHTVLDRIAGDQSTLQRYYVYNSVSYSAG
	l		VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL
			LGLCT
6821	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
ĺ		-	RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
İ			FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
1		i	GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
			GSVIEVLORRQEGLAS
6822	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTOHGPSPTVHPIOSPQN
			RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
			FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
		,	GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
			GSVIEVLORROEGLAS
6823	654	221	PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC
			GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE
1			YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL
L			ILRKGVLALNPLL
6824	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG
			ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV
		į	NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS
			LLRDPSKRKVPPOPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV
			WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS
		<u>. </u>	AALHICHAVILLQLWLGPQPFPKSTQHSKKAH
6825	3	1173	SSGEFGLOASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL
			PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ
			NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM
1			KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI
1		}	GIFSGYVDNFDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD
			IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF
			VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK
İ			TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF
L_			PFGPLALPMDGYGDSLWEEHEYKFCLALVISTKLYHVRC
6826	2304	954	LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPREYDTP
			LYFEEDEVRYLOSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA
			NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW
1			DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRSN
			AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLARAGI
	,		PTSSVFALHFTEPPISACLLAFLRVFCMTEEELKEHLLGDSAID
			RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIEEDKS
1			VLKNHDLSVRAKMAIKLRLGEKEILEKAVKSAAVNREYYRQQME
1			EKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEEEAGVQDALNI
			REAISKAKATENGLVNGENSIPNGTRSENESLNQESKRAVEDAK
1			GSSSDSTAGVKE
	L		GOODOTAGVE

SEO	Predicted	Predicted end	This is the same of the same o
ID	beginning	nucleotide	Amino acic segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	corresponding to first	1
1.	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	1
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
[amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion
6827	secuence	779	\=possible nucleotide insertion) .
0021	1	179	SSVVEFGLSVLGGLFLLFVLENMLGLLRHRGLRPRCCRRKRRNL
1	!		ETRNLDPENGSGMALOPLQAAPEPGAQGQREKNSOHPPALAPPG
1		:	HQGHSHGHQGGTDITWMVLLGDGLHNLTDGLAIGAAFSDGFSSG
1		į	LSTTLAVFCHELPHELGDFAMLLQSGLSFRRLLLLSLVSGALGL
}	}	:	GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALVEMLPALFPSS
(000		1	GAPAYA\HVLLQGLGLLLGGCLMLAITLLEERLLPVTTEG
6828	3	1654	KSQHG/WILOLMHSCKEGYVKDLKGNPGLHRAMLDLDNGTRFSE
ł			LGHLSQTASLKRGSSFQSGRDDTWRYKTPHRVAFVEKLTKLVLS
1			QLPNFWKLWISYVNGSLFSETAEKSGQIERSKNVRQRQNDFXKM
1	1	•	IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEVKCELSGQWLA
1	}	:	HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLRVRCVMATLQH
1 .			TAEEIKRLAEKEDWIVDNEGLTSLPCQFEQCIVCSLQSLKGVLE
	1	1	CKPGEASVFQQPKTQEEVCQLSINIMQVFIYCLEQLSTKPDADI
	1		DTTHLSVDVSSPDLFGSIHEDFSLTSEQRLLIVLSNCCYLERHT
1		1	FLNIAEHFEKHNFQGIEKITQVSMASLKELDQRLFENYIELKAD
1			PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKEALVNIIAVHAEV
1		1	FTISKELVPRVLSKVIEAVSEELSRLMQCVSSFSKNGALQARLE
İ		[ICALROTVAVYLTPESKSSFKQALEALPQLSSGADKKLLEELLN
		1	: KFKSSMHLQLTCFQAASSTMMKT
6829	1	782 .	MRMEAGEAAPFAGAGGRAAGGWGKWVRLNVGGTVFLTTRQTLCR
	<u> </u>	1	EQKSFLSRLCOGEELQSDRDETGAYLIDRDPTYFGPILNFLRHG
1	· ·	į	KLVLJKDMAEEGVLEEAEFYNIGPLIRIIKDRMEEKDYTVTQVP
1	ł		PKHYYRVLQCCEEELTQMVSTMSDGWRFEQLVNIGSSYNYGSED
1	i		QAEFLCVVSKELHSTPNGLSSESSRKTKSTEEQLEEQOQQEEEV
6830			EEVEVEOVOVEADAOEK/CCYKPEAPGCEAPDHLOGLGVPI
0030	1 3	935	MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL
1	1		RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR
		1	CFKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI EGSQGCENPKFSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL
		ł	RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT
-	l	{	ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE
1	Ì		DRGPRPGSPSALLPGPGRPPPPPTKPPETEAORGPCLQWLSEWT
1	Į		LEPDS
6831	3	1087	SLFFGSSTPDNKVAEOEDLETOPSPSVEKAVTVIDPEGTIPTNF
""	1	100/	NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGONVKEKSMILSN
	1	i	VEDLOOPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL
	1		EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI
	1		SIFKEEPRSDOKOKSLLSFDVVDKVPQQPKSASSNFASKNITKE
	l	i	SEKPESIILPVEESKGSLIDFSEDRLKKEMONPTSLKISEEETK
	ļ		LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKONSV\APLELRDS
	1	Į.	NEIGKTOITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG
	1	į	SEKEKDEKKKK
6832	1809	412	MGSGLISGPPCDNSGEALKEPERAQEHSLPNFAGGOHFFEYLLV
"""	1009	312	VSLKKKRSEDDYEPI1TYQFPKRENLLRGQQEEEERLLKAIPLF
	1		CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG
1	i		PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL
1	1		· · · · · · · · · · · · · · · · · · ·
	1	İ	REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL
	(i	LHCLSFEQILOIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVOMRFOOEVMDSPME
	1		1 77
	1		EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT
	1		AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK
İ	1	1	ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFOOKILE
-(633	<u> </u>		YEEQKKQ/TETKGKNCEIRAVVNKND
6833	i	1129	PLMTLSQCGG1 PGHGHSHGGHGHGHGLPKGPRVKSTRPGSSDIN
	}		VAPGEQGPDQEETNTLVANTSNSNGLKLDPADPENPRSGDTVEV
i	1	·	QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alamine, C=Cysteine, D=Aspartic Acid, E=
No:	nuclectide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location .	corresponding	H=Histidine, I=Isoleuc:ne, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acić	residue of	S=Serine, T=Threonine, V=Valine,
į.	residue of	amino acid	W=Tryptcphan, Y=Tyrosine, X=Unknown, *=Stop
ł .	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	<u> </u>	\=possible nucleotide insertion)
	1	i	NALVFYFSWKGCSEGDFCVNPCFPDPCKAFVEIINSTHASVYEA
1		ł	GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALILLQTVPKQID
-			IRNLIKELRNVEGVEEVHELHVWQLAGSRIIATAHIKCEDPTSY
1	1	}	MEVAKTIKDVFHNHGIHATTIQPEFASVGSKSSVVPCELACRTQ
1	1	•	CALKOCCGTLPQAPSGKDAEKTPAVSISCLELSNNLEKKPRRTK
			AENIPA\VVIEIKN\IPNK\QPESSL
6834	78	1151	AGOERPAPIWRLLWLPTPSVSRKAEPAHIPINR*GA*E*RGGLP
1		}	LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGP
1		1	CSKLVLSGARGIVGTTVQVLVEAQQPLLLLFTGVWGLNLRAGEE
1]	SRAL*LIEEVTQVRDAHLGNAVVGCAQCLSQGQVGSALAKALLE
1	1	t	AAAAVRDCKEVLTVSGDKQQAEVSVRL+VRDVCVEEAGCVEFGQ
1	1	Į	AHGRPGLALAKGRGGTNEVEEQVOVDGVQKLVLSAHECHELVAG
1	1		QQDGEDQAARTRLLQAGAHSVAHGRRQGQAPCRPHQEAGVSCHE
1	1	(LQQVVGDAL+ARE+APQIIVLLLLEDVAQLRTGKKA+DLVVDVE
<u></u>	<u> </u>	<u> </u>	QLLRQL
6835	ت	834	GIPAADR\EASLELIKLDISRTFPNLC1FQQGGPYHCMLHSILG
1		ļ	AYTCYRPDVGYVQGMSFIAAVLILNLDTADAFIAFSNLLNKPCQ
į		ţ	MAFFRVDHGLMLTYFAAFEVFFEENLPKLFAHFKKNNLTPDIYL
ł			IDWIFTLYSKSLPLDLACRIWDVFCRDGEEFLFRTALGILKLFE
1			DILTKMDFIHMAQFLTRLPEDLPAEELFASIATIQMQSRNKKWA
1	i		QVLTALQKDSREMREGKSVPPTLRLQREFALGTNQSPMPRPLCC
6836	 	850	FRLTPGOPRRTDAL MSCGRPPPDVDGMITLKV\DNLTYRTSPDSLRRVFEKYGRVGDV
0030	2	820	YIPREPHTKAPRGFAFVRFHDRRDAODAEAAMDGAELDGRELRV
}	})	QVARYGRRDLPRSRQGRRHAAGPEAA/RYGRRSRSYGRRSRSPR
1		1	RRHRSRSRGPSCSRSRSRSRYRGSRYSRSFYSRSPYSRSRYSRS
1			PYSRSRYRESRYGGSHYSSSGYSNSRYSRYHSSRSHSKSGSSTS
	ļ	(SRSASTSKSSSARRSKSSSVSRSRSRSRSSSMTRSPPRVSKRKS
1			KSRSRSKRPPKSPEEEGOMSS
6837	1	1369	TDGAAVAGNPGSDYFPGGTAP/GGPRTRRF\SGTSSSGSKASGP
1			PNPPAQGDGTSLSPNYTLESTSGNDGKPVSGGGGRGRGRRKRDS
1			GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGET
1	}		RGAPTPHEKALTSPSWGKGAELLLGDQPDLIGSLDGGAKSDSSS
1)	PNVGEFASDEVSTSYANEDEVSSSSDNPQALVKASRSPLVTGSP
1	1	}	KLPPRGVGAGEHGPKAPPPALGLGIMSNSTSTPDSYGGGGGPGH
		1	PGTPGLEQVRTPTSSSGAPPPDE1HPLE1LCAOIOLQRQQFSIS
1			EDOPLGLKGGKKGECAVGASGAONGDSELGSCCSEAVKSAMSTI
1	1	l	DLDSLMAEHSAAWYMPADKALVDSADDDKTLAPWEKAKPQNPNS
ļ	!	1	KEAHDLPANKASASQPGSHLQCLSVHCTDDVGDAKARASVPTWR
	1		SLHSDISNRFGTFVAALT
6838	∃€	499	LTDTPPPKTHMIHHS1SDYKATLkCWALGFYPMEITLTWQQDEE
1	1	ļ	DQTRDMELVETRPAGDGTFQKWAAVVVPSGEE/Q/RYMCHVQHE
}	1	!	GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVMC
			RKKNSDRVSYSEAASSDHAQGSDVSLTACKV
6839	3	1195	AAPAGGGPDPEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIHG
}		l	RGNFPTLSVQPRQIRAGGPQHPGGAG\IHVHRVRLHGSAASHVL
}	1	1	HPESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAGV
1	İ	1	SRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVELK
}	1	Ì	FVDSVRRQFEFSIDSFQIILDSLLLFGQCSSTPMSEAFHPTVTG
]	1	ESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLKYCHLLVRGFR
1	į	l	PRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLERYLEAHFGGAD
Į.		l	AARRYACLVTLHRVVNESTVCLMNHERRQTLDLIAALALQALAE
[((QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTWLP
L	L		CN
6840	4254	2061	ELÇGDFSVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKEL
L	l		FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW

SEO	Fredicted	Predicted end	lumino acid segment containing signal services
ID	beginning	redicted enc	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glucamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	E=E:stidine, I=Isoleucine, K=Lysine,
ı	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
<u> </u>	amino acid	sequence	Coden, /=possible nucleotide deletion,
1	secuence	i	\=possible nucleotide insertion)
 	acquence	-	TDI PVAMEHQPPYI IAVLPRYVEIRTFEPRLLVOSI ELORPRFI
1	Ì		TSGGSNIIYVASNHFVWRLIPVPMATQIQQLLQDKQFELALQLA
1			EMKDDSDSEKQQQIHHIKNLYAFNLFCOKRFDESMOVFAKLGTD
	1		PTHVMGLYPDLLPTDYRKOLOYPNPLFVLSGAELEKAHLALIDY
1			LTOKRSQLVKKLNDSDHQSSTSPLMEGTFTIKSKKKLLOIIDTT
İ			LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKYSELII
}		į	LYEKKGLHEKALOVLVDOSKKANSPLKGHERTVOYLOHLGTENL
Ī)		HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN
ł	1		FKGLAIPYLEHIIHVWEETGSRFHNCLIOLYCEKVOGLMKEYLL
			SFFAGKTPVPAGEEEGELGEYRQKLLMFLEISSYYDPGRLICDF
	1	[PFDGLLEERALLLGRMGKHEOALFIYVHILKDTRMAEEYCHKHY
	1	İ	DRNKDGNKDVYLSLLRMYLSFPSIHCLGPIKLELLEPKANLQAA
	{		LOVLELHHSKLDTTKALNLLFANTQINDIRIFLEKVLEENAOKK
	1		RFNOVLKNLLHAEFLRV\QEERILHQOVKCIITEEKVCMVCKKK
			IGNSAFARYPNGVVVHYFCS\KEVNPADT
6841	î	3206	TESTIGTKSNIPTSSVPSAAVTPLNESLOPLGDYGVGSKNSKRA
ļ]	REKRDSRNMEVQVTQEMRNVSIGMGSSDEWSDVQDIIDSTPELD
l	1		MCPETRLDRTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD
	1		VDFG/DLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIA
ł		ĺ	KVDOLSGEQEVLRGELEAAKQAKVKLENRIKELEEELKRVKSEA
1			IIARREPKEEAEDVSSYLCTESDKIPMACRRFTRVEMARVLME
1		į	RNOYKERLMELQEAVRWTEMIRASREHPSVQEKKKSTIWQFFSR
]	LFSSSSSPPPAKRPYPSGNIHYKSPTTAGFSQRRNHAMCPISAG
ì			SRPLEFFPDDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA
1 .	1		AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS
1			PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD
İ			QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDPGADGV
l	İ	ĺ	LAG1TLVGCATRCNVPRSNCSSRGDTPVLDKGQGEVATIANGKV
1		1	NPSOSTEEATEATEVFDPGPSEPETATLRPGPLTEHVFTDPAPT
ł		}	PSSGPOPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMWLG
	1		AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD
1	1		GTLA1FHRGEDGQWDLSNYHLMDLGHPHHS1RCMAVVYDRVWCG
	1		YKNKVHVIQPKTMQIEKSFDAHPRRESQVRÇLAWIGDGVWVSIR
	1		LDSTLRLYHAHTHQHLQDVDIEPYVSKMLGTGKLGFSFVRITAL
1	1	}	LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP
		ļ	TSGEG\ARPGG\IIHVYG\DDSSDRAARSFIPYCSMAQAQLCFH
			GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVEGQ
	1	1	KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVLSKA
6842	3	926	ERSELI VWOVSYTPE
0042	j	326	RCOCLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKP RRLFOSVKLHCPKCHLLQEVPHEGDLDIIFODGATKTPDVKLQN
]	1	TSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGT
1	1		LSE1CKLSNKFNSVIPVRSGHEDLELLDLSAFFLIQGTVHHYGC
]	KOWST* RSIQNLNSLVDKTSWIFSSVAEALGIVPLQYVFVMTFT
1			LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFC
1	1	ļ	PPG1K1DAYPWLECF1KSYNVTNGTDNQ1CYQIFDTTVAEDVI
€843	2	851	NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRIHTGERPYECSE
"""	1		CGRSFAENSSLIKHLRVHTGERPYECVECGKSFRRSSSLLOHOR
1			VHTRERPYECSECGKSFSLRSNLIHHORVHTGERHECGOCGKSF
1	}	1	SRKSSLITHLRVHTGERPYECSDCGKSFAENSSLIKHLRVHTGE
1	ļ		RPYECIDCGKSFRHSSSFRRHORVHTGMRPYK*SKFWKFSCPGF
			LLLOGORVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE
i	1		CNECEKAFSPLSLVTTIFT
6844	244	642	EHOLAGFELRKTQTSMSLGTTREKTDRVKSTAYLSPQELEDVFY
]		QYDVKSEIYSFGIVLWEIATGDIPFQGCNSEKIRKLVAVKRQQE
I	<u> </u>		The state of the s

SEC	Predicted	Predicted end	I have no noted gooment contact of an along the same
ID	beginning	1	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alamine, C=Cysteine, D=Aspartic Acid, E=
NO:		location.	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histicine, l=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino aciò	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
-			PLGEDCPSELREIIDECRAHDPSVRPSVDEILKKLSTFSK*CIK
			1
6845	3	1515	VAVRDECYNRHVFWDQDLWMLLFILMCHPETARARLEYRIRTLD
			GALENAQNLGYQGAKFAWESADSGLEVCPEDIYGVQEVHVNGAV
			GLAFELYYHTTQDLQLFREAGGWDVVRAVAEFWCSRVEWSPREE
	1)	KYHLRGVMS PDEYHSGVNNSVYTNVLVQNSLRFAAALAODLGLP
			IPSOWLAVADKIKVPFDVEONFHPEFDGYEPGEVVKOADVVLLG
		l I	YPVPFSLSPDVRRKNLEIYEAVTSPOGPAMTWSMFAVGWMELKD
			AVRARGLLDRSFANMAEPFKVWTENADGSGAVNFLTGMGGFLQA
ł	,		VVFGCTGFRVTRAGVTFDPVCLSGISRVSVSGIFYCGNKLNFSF
1			SEDSVTVEVTARAGPWAPHLEAELWPSQSRLSLLPGHKVSFPRS
			AGRIQMSPPKLPGSSSSEFPGRTFSDVRDPLQSPLWVTLGSSSP
i	}		TESLTVDPASE*SGTGASETSLGPSLWFRLHPPLLGTLLACHPS
1			PAARLSGKVHAAWPEFKAFCL
6846	213	1258	LYFLKTIK*LNRLAEHP*YENEKLTKLRNTIMEQYTRTEESARG
1 0010		1250	IIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKP
1	Į.		MTONEOKEVISKFRTGKINLLIATTVAEEGLDIKECNIVIRYGL
Í		ļ	VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKM
1			MYKAIHCVCNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYK
Ì	1	1	NNPSLITFLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELYIV
			RENKTLOKKCADYOINGEIICKCGOAWGTMMVHKGLDLPCLKIR
}	}	}	NFVVVFKNNSTKKQYKKWVELFITFPNLDYSECCLFSDED
6847	1450	346	SMCWNSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT
004/	1450	348	
		•	WFEDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ
	į		PFAYGTLTVRSLLDTREHCLNEFNFPDPYSKVKQRENGVALRCF
1		Ì	PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP
			YFGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG
1	<u> </u>		IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE
			RIAGMDPVVHSALREERLLLVOTGSSSPCLDLSRLDKGLAALVR
l			ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG
6040			GRLFSVIFKYEVPAE
6848	19	16	AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND
	}	1	LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH
		Ī	IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN
1	[\	VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK
1	1	[VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPODLGTA
L			YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH
6849	70	821	SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHOSYEC
1	İ	İ	VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK
1]]	PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM
	J		VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVJGAQKPQ
1	1	j	YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG
			VIKVKGKGQLCTYFLNTDLTRTGPPSATLG
6850	2	1235	ARGUNHEWTFEKLROHISRNAODKOELHLFMLSGVPDAVFDLTD
		I	LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL
[1	1	RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI
	1	i	GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT
	!		KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
1		ſ	NNIRTIEE11SFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL
		i	YFSNNKLESLFVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ
	ļ	ļ	HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ
			LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK
	1		EALNQDINIPFANGI
6851	1765	660	VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD
1			LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA
1	}	1	CYCVYKLTIGRDDSEKLEEEGEEEWDDDQELDEEEPDIWFDFET
			<u> </u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
IE.	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid		Codon, /=possible nucleotice deletion,
		sequence	
	seguence .	<u> </u>	\=possible nucleotide insertion)
		1	MARPWTEDGDWTEPGAPGGTEDRPSGGGKANRAHPIKORPFPYE
	}	1	HKNTWSAQNCKNGSCVLDLSKCLFIOGKLLFAEPKDAGFPFSQD
		į	INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESOGQIKM
			YINEVCRETVSRCCNSFLQQAGLNLL:SMTVINNMLAKSASDLK
	{		FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLFSFMSL
			FIRNGNREILLETPAP
6852	1	407	RTRGEETYANFIKHNDGKNIFYAARTFATLFAVMFAMYIISGLT
	ļ		GFIGLNSIAVLCNLVMGLALIFLCTWAYVKYSGEFREIGTVIDQ
			IAETLWEQVLKPLGDNLMEENIRQSVTNSIKAGLTDOVSHHARL
		ļ	KTD
6853	3	469	GDSCAVCIELYKPNDLVRILTCNHIFEKTCVDPWLLEHRTCPMC
	:		KCDILKALGIEVDVEDGSVSLQVPVSNEIFNSASSHEEDNRSET
	{		ASSGYASVQGTYEPPLEEHVQSTNESLQLVNHEANSVAVDVIPH
	}		VDNPTFEEDETPNQETAVREIKS
6854	1148	585	HESYIGTFDPGELCVCAAIOWLODNSASYFLNRKLVYEFSTOAK
			PVKNTFLRMWIYSHHIYQQDLRKKILDVGKRLDVTGFCMTGKPG
			11CVEGFKEHCEEFWHT1RYPNWKH15CKHAESVETEGNGEDLR
			LFHSFEELLLEAHGDYGLRNDYHMNLGOFLEFLKKHKSEHVFQI
	1		LFGIESKSSDS
6855	1913	1148	GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDOTDDLAK
0000	1913	1140	EEPTSLFORDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF
		1	
			YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHI
	1	1	QLTYFSRWSEVEDSCDSDAIERMYCAPEVGAITEETEACDWWSL
			GAVLFELLTGKTLVECHPAGINTHTTLNMPEWVSEEARSLIQQL
			LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR
6856	1617	997	VTOLYVSVDASTKDSLKKI DRPLFKDFWQQFLDSLKALAVKQQR
		ĺ	TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA
			SSLTMAHVPWHEEVVQFVRELVDLIPEYEIACEHEHSNCLLIAH
			RKFKIGGEWWTWINYNRFOELIQEYEDSGGSKTFSAKDYMARTP
		<u> </u>	HWALFGASERGFDPKDTRHQRKNKSKA1SGC
6857) <u>1</u>	617	KGPEATAMVCVCSHPNCRONHIKPSHSAAQTWCGSPTPASAPNH
		1	KLMAMEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF
			DLQORLSDEDGTNMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT
	į		TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSFLCKAF
			RHVKVDTLSQPEALSRILVPAAWCTVGRD
6858	-2	669	RSRGIKDFENDPPLSSCG1FQSRIAGDALLDSGIRISSVFASPA
			LRCVOTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM
			SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ
		1	IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR
			KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS
]	GN
6859	1	1150	GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG
	_		KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE
	}		AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT
	1	1	SSASWVAGSFSPVSPPVVDLRTIMEIEESROKCGATPKSHLGKT
			VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN
			AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN
			SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM
		1	
			VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIGDLLVF
	l	<u> </u>	YEAFGNPEEFVIVERTPOGPLAVPMWNKHGC
6860	1889	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
		1	DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP
		}	MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
		T	THE PARTY OF THE P
6861	1889	1515	DKDKKROKKRGIFPKVATNIMRAWLFOHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSFEGQP

SEO I	Fredicted	Predicted end	Limino soid coment containing cional montide
ID	beginning	nucleotice	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
, ,,,	location	corresponding	H=Histidine, I=Isoloucine, K=Lvsine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino ació	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence.	\=possible nucleotide insertion)
<u> </u>	- Cequence	 	MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6862		471	EEI DREFHNKLKLKEDKLEKOEKPVNGEDKGDSGVDTONSEGNA
0002	•	3/,	DEEDPLGPNCYYDKTKSFFDNISCDDNRERRPTWAEERRLNAET
			FGIPLRPNRGRGGYRGRGGLGFRGGRGGGRGGTFTAPRGFRG
i			GFRGGRGGREFADFEYRKTTAFGP
6863	2216	487	POEPALKSEFSOVASNTIPLFLPOPNTCKONGPCKOVCSTVGGS
0003	2210	36,	AICSCFPGYAIMADGVSCEDCDECLMGAHDCSRROFCVNTLGSF
]			
! !		į	YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL
			GSFHCYKALTCEPGYALKDGECEDVDECAMGTHTCQVGFLCQNT
j l			KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI
			NTVGSYTCQRNPLICARGYHASDDGTKCVDVNECETGVHRCGEG OVCHNLPGSYRCDCKAGFORDAFGRGCIDVNECWASPGRLCOHT
			CENTLGSYRCSCASGFLLAADGKRCEDVNECEAORCSQECANIY
			• •
[GSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILCTFRCLNVPGS YOCACPEOGYTMTANGRSCKDVDECALGTHNCSEAETCHNIOGS
			FRCLRFECPPNYVOVSKTKCERTTCHDFLECONSPARITHYOLN
[POTGLLVFAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLN
			AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT
	·	Ĭ	TFAL
6864	2	2933	LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSSG
[550.]	-		FVGLRNGGATCYMNAVFOOLYMOPGLPESLLSVDDDTDNPDDSV
[FYOVOSLFGHLMESKLOYYVPENFWKIFKMWNKELYVREOODAY
			EFFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSDQKICKDCPHRY
			EREEAFMALNLGVTSCCSLEISLDQFVRGEVLEGSNAYYCEKCK
			EKRITVKRTCIKSLPSVLVIHLMRFGFDWESGRSIKYDEQIRFP
i i		İ	WMLNMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPRKKVALT
			ENYELVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWYKFNDTVIE
			EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAYMLFY
ļ :			QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPÇSSPR
			PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYOMVRDENLKF
			MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLQLAIQ
			FLFQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQWLVEYFIS
<u> </u>			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYODKLKSL
			HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL
			LRHSALRHMISFLLGASRONNQIRRWSSAQAREFGNLHNTVALL
			VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM
			SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN
			GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH
1			WSWAVQNLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA
			YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL
			RSDLDDVDP
6865	1820	1242	DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS
j			CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV
			LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ
(DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS
i		L	PFGQSSVQTIQPKRDS
6866	1571	495	DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF
[IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP
			AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG
			SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR
			VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV
			IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL
			GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF
			QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL
			EMAQLH
			1 -

SEQ	Predicted	Predicted end	Amino acid secment containing signal peptice
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NG:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, l=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acic	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	Į.	
1	sequence	seguence	Codon, /=possible nucleotide deletion,
6867	2833	1704	\=possible nucleotide insertion)
6067	2833	1704	GTRIMSQPKQKELAGFVRQXMLLDYSVYMGRCVPQESRSPORSP
i			LQSAESSPTAGKKLPEVPPSEEEEQEAWVNALLGRIFWDFLGEK
l	İ		YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILQAF
<u> </u>	ļ		KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK
}			VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKQL
1			LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEFIKKKIEE,
1	ļ		VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVWYGFRKPPHVELK
1	1		ARPKLGEREVTLVHVTDWIEKKLEQEFOKVFVMPNMDDVYITIM
	L		HSAMDPRSTSCLLKDPPVEAADQP
686€	1	341	RPTRPPTRPEEIKNLILPY1SDMNFVQDLCEDFYELFKTDKGFD
			KATFESOMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG
		<u>L</u>	GSQGRIVHLSNSFTQTVNCRKPFFSSW
6869	3	1619	MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES
1	1		KEISVEKSLYKEIQOCLVGNKGIEVFYKIQEDVYETLKDRYYPS
1	1	1	FIVSDLYEKLLIKEEEKHASOMISNKDEMGPRDEAGEEAVDDGT
1			NQINEQASFAVNKLRELNEKLEYKRQALNSIQNAPKPDKKIVSK
1	,		LKDEIILIEKERTDLOLHMARTDWWCENLGMWKASITSGEVTEE
1	}		NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHRKLSEC
1			VPSLKKDQLPSLSKLPFKSIDHTFMEKFENQLNKFLQNLLSDER
1			LCQSEALYAFLSPSFDYLKVIDVQGKKNSFSLSSFLERLPRDFF
i			SHQEEETEEDSDLSDYGDDVDGRKDALAEPCFMLIGEIFELRGM .
1			FKWVRRTLIALVQVTFGRTINKQIRDTVSWIFSEQMLVYYINIF
1			RDAFWPNGKLAPPTTIRSKEOSQETKQRAQQKLLENIPDMLQSL
i	Ì		VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV
i			HLDQLKAGQV
6870	1	156£	MAAVVAATRWWQLLLVLSAAGMGASGAPQPPNILLLLMDDMGWG
1			DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANPLCSPSRAALLT
	j		GRLPIRNGFYTTNAHARNAYTPQEIVGGIPDSEQLLPELLKKAG
1			YVSKIVGKWHLGHRPQFHPLKHGFDEWFGSPNCHFGPYDNKARP
}			NIPVYRDWEMVGRYYEEFPINLKTGEANLTQIYLQEALDFIKRQ
			ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDAVREIDDS
1			IGKILELLQDLHVADNTFVFFTSDNGAALISAPEQGGSNGPFLC
	!		GKQTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLAL
			AGLTPPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATLG
1			QHKAHFWTWTNSWENFRQGIDFCPGQNVSGVTTHNLEDHTKLPL
į			IFHLGRDPGERFPLSFASAEYQEALSRITSVVQQHQEALVPAQP
<u></u>			QLNVCNWAVMNWAPPGCEKLGKCLTPPESIPKKCLWSH
6871	209	112€	RMSLNPP1FLKRSEENSSKFVETKQSQTTS1ASEDPLQNLCLAS
]		QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPVENVPIEQIPLV
1			KLPLKIDIIKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPEYE
			EKDHEVALIFPGPQSISIKDISFHLQKRIQNNVRGKNDDPDKPS
1			FKRKRTEEQEFCDLNDSKCKGTTLKKIIFIDSTWNQTNKIFTDE
1			RLQGLLQVELKTRKTCFWRHQKGKPDTFLSTIEAIYYFLVDYHT
			DILKEKYRGQYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
6872	880	459	FGLLMVVLSL1FMKGNCVREDL1FNFLFKLGLDVRETNGLFGNT
1			KKLITEVFVRQKYLEYRRIPYTEPAEYEFLWGPRAFLETSKMLV
			LRFLAKLHKKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAHG
L			PTSRPPPR
6873	1929	955	DEQAVLCSKDKTYDLKIADTSNMLLF1PGCKTPDQLKKEDSHCN
1	1		IIHTEIFGFSNNYWELRRRRPKLKKLKKLLMENPYEGPDSQKEK
1			DSNSSKYTTEDLLDQIQASEEEIMTQLQVLNACKIGGYWRILEF
1	1	•	DYEMKLLNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIEH
			CLKCYGKKYVDEGEVYFELDADKICRAAARMLLQNAVKFNLAEF
	Į į		QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLPE
			DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYSH
			SSMQNGVKVYNSRRPIS
L	<u> </u>		1

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amono acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide		
NO:	1	location	Glucamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Froline, Q=Glutamine, R=Argininc,
1	amino acid	residue cf	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Cocon, /=possible nucleotide deletion,
1	sequence		\=rossible nucleotide insertion)
6874	1 1	307	DS:ADHVNSAAVNVEEGTKNLGKAAKYKLAALPVAGALIGGMVG
			GPJGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKCKMMEKLTS
1			SCI-DLPSOTDKKCS
6875	3.606	349	1
00/5	1688	343	VIGTGERGNSASEKWEIMFNEELGDPFIIIHSISLLNAEEHSIA
}		<u>'</u>	TLLLRIEKEELDMKGSGFYVSLEWVTISKKNQDNKKYEIIKRDI
[}	LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI
1		1	SEKTKEPLYYWQQTEDDLTVTIRLPEDNTKED1Q1QFLPDHINI
1	1	1	VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW
	l		PELVIGDKQGELIRDSAQCAAIAERLMHLTSEELNPNPDKEKPP
	Ì	Í	CNAQELEECDIFFEESSSLCRFDGNTLKTTHVVNLGSNQYLFSV
1	ļ		IVEPKEMPCFCLRHDVDALLWQPHSSKQDDMWEHIATFNALGYV
1	Ì	-	QASKRDKKFFACAPNYSYAALCECLRRVFIYRQPAPMSTVLYNR
1	1		KEGROVGOVAKOOVASLETNDPILGFOATNERLFVLTTKNLFLI
İ)	KVNTEN
6876	41	1285	VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS
1 5575	3.	1203	LHTKPRMPPCDFMPERYOVIFLVNSGSEANELAMLMARAHSNNI
1	1		DIISFRGAYHGCSPYTLGLTNVGIYKMELPGGTGCOFTMCPDVF
ļ.			
ł			RGPWGGSHCRDSPVQT1RKCSCAPDCCQAKDQY1EQFKDTLSTS
1			VAKSIAGFFAEPIQGVNGVVQYPKGFLKEAFELVRARGGVCIAN
1			EVCTGFGRLGSHFWGFOTHDVLPDIVTMAKGIGNGFFMAAVITT
İ		İ	PEIAKSLAKCLQHFNTFGGNPMACAIGSAVLEVIKEENLQENSQ
1			EVGTYMLLKFAKLRDEFEIVGDVRGKGLMIGIENVQDKISCRPL
	1		PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMC17KPEVDF
1	ļ	l	AVEVFRSALTOHMERRAK
6877	3	778	GTSFSPARAYAPPTERKRFYONVSITQGEGGFEINLDHRKLKTP
1		1	QAKLFTVPSEALAIAVATEWDSQQDTIKYYTMHLTTLCNTSLDN
ļ		•	PTORNKDQLIRAAVKFLDTDTICYRVEEPETLVELQRNEWDPII
1		ł	EWAEKRYGVEISSSTSIMGPSIPAKTREVLVSHLASYNTWALQG
			IEFVAAQLKSMVLTLGLIDLRLTVEQAVLLSRLEEEYOIQKWGN
}			IEWAHDYELQELRARTAAGTLFIHLCSESTTVKHKLLKE
6878	935	263	QTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAFSEQGON
	1	1	LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAP
		ļ	EYTWFKDGIRLLENPRLGSOSTNSSYTMNTKTGTLQFNTVSKLD
1	1		TGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
İ			The state of the s
i		}	VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF
1		 	11
6879	3	845	IRVIGESDIMQEFLSESDENYNGVSDVELRVALPDGTTVTVRVK
1	1]	KNSTTDQVYQAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE
1		Į.	FPHKLY10NYTSAVPGTCLT1RKWLFTTEEE1LLNDNDLAVTYF
1	·		FHCAVDDVKKGYIKAEEKSYQLQKLYEQRKMVMYLNMLRTCEGY
1		l	NEI]FPHCACDSRRKGHVITAISITHFKLHACTEEGOLENQVIA
1	1	1	FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVK1FTPYFNYMHE
1			CFERVFCELKWRKEEY
6880	2110	1437	RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS
			MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS
1			NRDC: KNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH
			VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS
i		İ	KPCVPEYAPROERIRDLSGNLWERSSGDGEELERLTKPKSDESD
1		ļ	1
6000	 	 	EDT7
6881	263€	2244	NDSKWEDJHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR
}	1		QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYQS
<u> </u>	<u></u>		IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR
6882	1	850	GIPFAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN
1	1		QEGNMVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT
i	1		TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH
ļ	1		MRPERPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK
<u> </u>	<u> </u>	L	

SEQ	Fredicted	Predicted end	Amino acid segment containing signal peptide
1		1	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Fhenylalanine, G=Glycine,
ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	b=beucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	
1	•		S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	1	\=possible nucleotide insertion)
 	i	 	KVKATNFRENIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI
ł	i -	1	LTTVDPDTGVMSRKEPLETLKSYROCDPSERKLYGKSPLFGOYF
ì		ţ	
L	<u> </u>		VLENPGTIKVGDPVYLLGC
6883	2794	2256	NEKLKLNONLKLFITLTYCVLSLHGWGPGIHLQKEGAFPVTQNR
ł	1	1	ALOLLYDLRYLNIVLTAKGDEVKSGRSKPDSRIEKVTDHLEALI
1	i .		DPFDLDVFTPHLNSNLHRLVORTSVLFGLVTGTENOLAPRSSTF
	1	1	NSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYD
	1	1	
	L		ANC
6884		99	EFERVTAEAVKPRETSEPRAAAQRFCEKFPFL
6885	297	1554	STGOFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFGDV
j	}	}	LCDSPYQLILSAFDFIKNSGQEASFMIWTGDSPPHVPVPELSTD
1	1	1	TVINVITNMTTTIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV
1		l	YNAVANLWKPWLDEEAISTLRKGGFYSOKVTTNPNLRIISLNTN
1	1		
1	1		LYYGPNIMTLNKTDPANQFEWLESTLNNSQONKEKVYIIAHVPV
1	1	1	GYLPSSONITAMREYYNEKLIDIFOKYSDVIAGOFYGHTHRDSI
	1	1	MVLSDKKGSPVNSLFVAPAVTPVKSVLEKCTNNPGIRLFQYDPR
1	1	1	DYKLLDMLCYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPES
i	ł	1	LYGLAKOFTILDSKOFIKYYNYFFVSYDSSVTCDKTCKAFOICA
1		1	IMNLDNISYADCLKOLYIKHNY
		l	· · · · · · · · · · · · · · · · · · ·
6886	2	1341	QCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK
1	1	I	QARVSQELKKAAKRTVSISEGPDTLGDGMRERRETLALAPEPEP
		1	LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDFKKRRGHSI
1		1	GGAPEORYCI I PVCVAARLPTRAQDVLDAHLSEVNAVRFGPNSS
1	1	ł	LLATGGADRLIHLWNVVGSRLEANQTLEGAGGSITSVDFDPSGY
}	1	j	QVLAATYNOAAQLWKVGEAQSKETLSGHKDKVTAAKFKLTRHQA
1		İ	VIGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN
	ľ		
}	ł.	1	DOKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDQLHLLSCSRDNT
		ļ	LKVIDLRVSNIRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD
1		1	GALY I WDVDTGKLESRLQGPHCAAVNAVAWCY SGSHMVSVDQGR
}	1		KVVLWO
6887	1047	116	WTARPSQKFFWEAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHG
1	1	1 -20	GOGRAAGPTLPRGERGGPOOSGPGLAAQTPPTSKQVAWRAFLTG
1			TYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVY
(ļ		NASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLT
l .			FASNNVTDMFPDLPFTDELRQRYCLDTWGVWPRPDWLLTSFWGG
1			DLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHHLD
1		1	LEASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRL
J.		1	Si.
6888	 		FVAYVKKEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI
1 6999	1	992	
ł	1	}	NF1KGRAPNHRLFQAFFEE1G1EYSVLLFHTEMRWLSRGQILTH
1	1		IFEMYEEINOFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE
1	Į.		LSASMORTGMNTVSAREKLSAFVRKFPFWOKRIEKRNFTNFPFL
1	İ	1	EE1:VSDNEGIFIAAE1TLHLQQLSNFFHGYFSIGDLNEASKW1
i	1	1	LDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC
i	Ī		
1			AOFTAFPNLAKTALEILMPFATTYLCELGFSITFTFQNKVPEAA
	1		LILSDDIRVAISKKVPSFLGHH
6889	3	1534	LTLENQIKEEREQDNSESPNGRTSPLVSONNEQGSTLRDLLTTT
1			AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV
1			ENKI PPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW
1	1	J.	
1			ICEKHILWLKDYKNSSNWKLFKECWKOGQFAVVSGVHKKMNISL
1	1	1	WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ
1			KNKSGETVVLKLKDWPSGEDFKTMMPARYEDLLKSLPLPEYCNP
1		1	EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI
1	1		EVSDVVNILVYVGIAKGNG:LSKAGILKKFEEEDLDDILRKRLK
	Ì	1	
			DSSEIPGALKHIYAGKOVDKIREFLOKISKEQGLEVLPEHDPIR DOSWYYNKKLRORLLBEYGVRTWTLIQFLGDAIVLPAGALHQVQ

SEC	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ĺ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
,	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	secuence		\=possible nucleotide insertion)
[NFHSCIQVTEDFVSPEHLVESFHLTQELRLLKEEINYDDKLQVK
1	1		NILYHAVKEMVRALKIHEDEVDDMEEN
6890	3	667	THACGMUI PLYLERALVVEKTAETCNSPPCGAKDSLIFGAITCF
			TGFLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV
l			AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAV
İ			ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA
{		1	LMLCPFVVVLGGMFFLATALFFVSDRARAEQQVNQLAMPPASVK
			V
6891	1980	1262	LRIHQELLSKELKLLRGITIESIIHIGLAAGKEQFMQDASNVMQ
1		1	LLLKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE
}	1	\	AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKFKPNCVNVD
ŀ			EVLPHWLSWLPLHEDKEEAIOTLSFLCDLIESNHPVVIGPNNSN
1	1	1	LPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLEC
j			VSQLDDEQQEALQELLNFA
6892	3	876	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV
5552	1	1 676	FALRAFNVELAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH
Į.		1	OPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNIKELE
}			NYAENTOSSLLYLTLEILGIKDLHADHAASHIGKAOGIVTCLRA
t]	TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDXNVRDVIYDIA
			l i
1			SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIQRVDFD
6893	1	842	1FHPSLQQKNTLLPLYLY1QSWRKTY
0033	1	042	DGERKSMSVERTFSEINKAEEQYSLCOELCSELAQDLOKERLKG
	j		RTVTIKLKNVNFEVKTRASTVSSVVSTAEEIFAIAKELLKTEID
			ADFPHPLRLRLMGVRISSFPNEEDRKHQQRSIIGFLQAGNQALS
í			ATECTLERTDRDRFVRPLEMSHKKSFFDKKRSERKWSHQDTFKC
		}	EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR
]		1	AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKE
6894	1 225	ļ	NVPASSLCEKQDYEAH
6694	1742	1463	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG
!			DVRDRGHGRPWQPSLEPSLFPTLCFPSLSSFSSSWPSAQHLTPS
6895	2226	 	VFNPW
6095	2379	478	VTYVELCDLASPTALLIMRTVLDLIVEDLQSTSEDKEQQYTSQT
]		l	TRLLALLYALASHKACKLATLHLINGTIKGDERYAETFQDLLAL
		1	VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISEL
]	İ]	EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL
		I	AEHDYGLFHLKSSLRKNSSALHSLLKRVVSTFSKDTGELASSFL
]]	1	EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKQLL
		1	QSKEESPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKQMLES
}	İ	1	SGDPLPLSDQDVEPVLSAPESLQNLFNNRTAYVLADVMDDQLKS
	1		MWFTPFOAEEIDTDLDLVKVDLIELSEKCCSDFDLHSELERSFL
		1	SEPSSPGRTKTTKGFKLGKHKHETFITSSGKSEYIEPAKRAHVV
	1	1	PPPRGRGGGGGGGIRPHDIFRQRKQNTSRPPSMHVDDFVAAES
}		1	KEVVPQDGIPPPKRPLXVSQKISSRGGFSGNRGGRGAFHSQNRF
		1	FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG
}	}	}	PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSGSGGSRG
	<u></u>		KFVSGGSGRGRHVRSFTR
6896	1	. 555	GNIVIQKKKYNKQHIIPLENVTIDSIKDEGDLRNGWLIKTPTKS
	1	1	FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD
1	}	·	SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSEKRFLLPSQ
	1		SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD
	!		DDDDDDSSD
6897	3	920	GDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASLNHY
	1		AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL
	1	!	SLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLA
		ļ	YLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDE
	1	1	DFVLVLAULHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML
	L	L	NI 1 P 1 THURNING CONTROL WALLING CONTROL I AND A SIGNIFIA

NO:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO: nucleotide location: corresponding corresponding to first lamino acid amino acid residue of residue of residue of residue of residue of amino acid sequence sequen				Amaino acid segment containing signal peptide
Coation Corresponding Leleucine, Memethicaine, Nebsparagine, Leleucine, Memethicaine, Nebsparagine, Leleucine, Memethicaine, Nebsparagine, Nesidue of amino acid sequence Seserine, Tetreronine, Vevaline, Nesidue of amino acid sequence Nesidue of amino acid sequence Nesidue of amino acid sequence Literackermine, Vevaline, Nesidue of amino acid sequence Nesidue of Amino acid sequence Literackermine, Vevaline, Nesidue of amino acid sequence Nesidue of Amino acid Nesidue of Am		1	!	
corresponding to first amino acid residue of residue of residue of residue of residue of residue of amino acid sequence amino acid sequence sequenc			•	
to first amino acid residue of residue of amino acid sequence sequence sequence sequence sequence sequence sequence LENFLAMEKORPHMEYECPYLLYVEVVAFILEPROGRAVPADE LENFLAMEKORPHMEYECPYLLYVEVVAFILEPROGRAVPADE LENFLAMEKORPHMEYECPYLLYVEVVAFILEPROGRAVPADE LENFLAMEKORPHMEYECPYLLYVEVVAFILEPROGRAVPADE LENFLAMEKORPHMEYECPYLLYVEVVAFILEPROGRAVPADE LENFLAMEKORPHMEYECPYLLYVEVVAFILEPROGRAVPADE LENGLAME OCCUPANY TENGLAME OCCUPANY TENGLAME OCFILESLAT/GOUTENER TENGLAME OCFILESLAT/GOUTENER TENGLAME OCFILESLAT/GOUTENER TENGLAME OCFILESLAT/GOUTENER TENGLAME OCFILESLAT/GOUTENER TENGLAME OCFILESLAT/GOUTENER TENGLAME OCFILESLAT/GOUTENER TENGLAME OCFILESLAT/GOUTENER TENGLAME OCFILESLAT/GOUTENER TENGLAME OCFILESLAT/GOUTENER TENGLAME OCFILESLAT/GOUTENER OCFILESLAT/GOUTENER OCFILESLAT/GOUTENER OCFILESLATION TO THE OCFILE OCFILESLATION TO THE OCFILE OCFI				
amino acid residue ci amino acid sequence (S-Serine TeThreonine, V=Valine, amino acid sequence (S-Serine, TeThreonine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, V=possible nuc	i i			
residue of amino acid sequence (Codon, /=possible nucleotide deletion, %=Stop Codon, /=possible nucleotide deletion, %=Stop Codon, /=possible nucleotide deletion, %=Ostop Lander of the first of the color of the co	!		i	
amino acid sequence Codon, /=possible nucleotide deletion,		* *	1	
Sequence \-possible nucleotice insertion LRLPLAMEKGRHMEYECPYLVYVPVNFRLEPKDGKGVFAVDGE LMVSEAVCGCVIPNNFMMVSGCVEPPSMKFOCMPPPEPL LMVSEAVCGCVIPNNFMMVSGCVEPPSMKFOCMPPPEPL LMVSEAVCGCVIPNNFMMVSGCVEPPSMKFOCMPPPEPL LMVSEAVCGCVIPNNFMMVSGCVEPPSMKFOCMPPPEPL LMVSEAVCGCVIPNNFMMVSGCVEPPSMKFOCMPPPEPL LMVSEAVCGCVIPNFMMVSGCVEPPSMKFOCMPPPEPL LMVSEAVCGCVIPNFMMVSGCVEPPSMKFMMVITIMGILMPA OGFLISLAFYGMTGCSLGFOSPRKEIQMESLTTSAAEGAHFSPL MPHENPASCKVSQVGGGTSDEALSMLSEGSDASTIEIHTASESC NKNEGDFALPTHGDL LEHGGEYTFSLPCAYARSILTVPWWSLGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSASI THEMPASE TILVPAMEWIGKWSVMCAKTGYSE TILVPAMEWIGKWSVMCAKTGYSE TILVPAMEWIGKWSVMCAKTGYSE TILVPAMEWIGKWSVMCAKTGYSE TILVPAMEWIGKWSVMCAKTGYSE TILVPAMEWIGKWSVMCAKTGYSE TILVPAMEWIGKWSMCATTH TILVPAMEWIGKMSTATH TILVPAM	j l		1	
LRIPLAMEKGRHMEYBCPYLVVVPVMFFILEPKDGKGVFAVDGE LMMSEAVOGOVHPNYFWMYSGCVEPPPSWKPOOMPPPEEPL 6896 919 346 OKTVTAVASLIKGRGGITTENERRMGAVINIRFFKIMLVLIICM LSNIINESLLFYLEMGTDINGGSLKPVMTAAKTTWFIMGILNPA OGFLISLAFYGWTGCSLGFOGFRKEIOWESLTTSAAEGAHPSPL MPHENPASGKVSQVGGGTSDELABMLSEGGDASTIEIHTASESC NKNEGDFALFTHODL 6899 120 827 MKVRKNDAVILDEKNKINMDCFISCFFKKMLITLMFSHSGILSL LEHGEEYTFSLPCAYARSILTVPWVELGGKVSVNCAKTGYSASI TFHTKPFYGGKLHRVTAEVKRNFILEKGOPFESRELMKVTDSLRGS NGETKYVDLTKLAUTYKKNFILEKGOPFESRELMKVTDSLRGS EIDKATEHKHTLSERGRTEGRERTETGTPWKTKYFIKEGDGWVY HKPLWKIIPTTQDAE 6900 3 451 TEVLGSKGHEERSSTSALHHALEESASLLTMFWRAALPSTHIP VLPGKVGESTERELLELETKVSQOEQLLOSTTEHLKNANQOGES MEGFIVSOLTRATHOUKKARTILEVRKLHQSEAPSLSPTHHPH LADLVGGSWBALRFOEK 6901 1 203 DDNMVQRLETDFKMTLQQOSTLEOMAWLDNVMQALKPYEGRP SFPKAAROFLLKKSFYRTHLOFS SPRADAPSLDLLPEITMPDELLSYLDPPDLSNSNADDLLSLFENN 6902 2 2667 GAPPPPPSOPPROPPQAARSSEPHSDLTFNFSSALEGOAGAGGA SDMPPPSLOLLPEITMPDELLSYLDPPDLSNSNADDLLSLFENN 6903 1 149 RINOVPKGSPTGIHTLVIDOWVQMPQDESCFLFSTVKAESSBGI HIILK CSGALVSSLATGLKPRYHFAALEKTYYLGRPYVLGANNQETVKYPQDA DGCELAENITYLGRKGIPTGSSGLQIVYYLSGTESLNEPVPPGYSF SPKDVSSLRMMLCTTSQFKGVEILLTSPWFKCVGMFGMSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYKNHIILDEN AQHATRIIALANVGNPEKKKYLYAFSI VPMKLMDAABLVLVQPDP VTENPYRKSGGEASIGKQILAFVEESACOFFPDLNEKQGRKRSS TGRDSKSSPHPKOPKKPROPPG-CWFCLASPEVEKHLVVNIGTH CYLALAGGGLSDHVLILIPIGHKYGSVVELSAEVEKEKKYTTL RRFFKSRGKWCVVFERNYKSHLLQLQVI PVPISCSTTDDIKDAF ITQAQGQOTELLEIPHSDIK GLAQGAAVFYVELDTGKLFHR IKKNFPLOFGREVLASEAILIVVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSCHGERETTISHYLFBLGVYRTLYLFNHWRYHFEGFFDLIAI VAGLVQVVLVCOFFYLYTIKVLKGKKLSLPA FRKDFEPYDFTLDD 40504 5906 501 226 5907 1 226 5908 51 226 5908 51 226 5908 51 5	1		sequence	
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HIILK 6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGI KXAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQILVYLSGTESLNEPVPGYSF SPKDVSSLRMMCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFILALNVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACOFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKÇIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNEFLNLAIPIVVFTET	6903	1	149	RINOVYROGPTGIHILVIDOMVONFODESCFLFSTVKAESSDGI
VGNFFGSTQDAEWEEYKTGI KXAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFI ALANVGNPEKKKYLYAFSI VPMKHMDAAELVKQPPD VTENPYRKSGQEASIGKQI LAPVEESACOFFFDLNEKQGRKRSS TGRDSKSS PHPKQPRKPPQPPGPCMFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVI PVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDI KÇI AQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNEFLNLAIPIVVFTET				1
DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKHMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACOFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKÇIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKTIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNEFLNLAIPIVVFTET	€904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVOAIOKKSGNFDLLLC
SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALIANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGGASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKÇIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLOFT FRKDFEPYDFTLSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET	1	Ì		VGNFFGSTQDAEWEEYKTG1KKAPIQTYVLGANNQETVKYFQDA
TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACOFFFDLMEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQGVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFENNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTULYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET				DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF
AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELUKQPPD VTENPYRKSGQEASIGKQILAPVEESACOFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDEVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNEFLNLAIPIVVFTET				SPKDVSSLRMMLCTTSQFKGVDILLTSPWPKCVGNFGNSSGEVD
VTENPYRKSGQEASIGKQILAPVEESACOFFFDLNEKQGRRRSS TGRDSKSSPHPKOPRKPPOPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKÇIAQPGAAYFYVELDTGEKLFHR IKKNFPLOFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNEFLNLAIPIVVFTET			İ	TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN
TGRDSKSSPHPKOPRKPPOPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKÇIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNEFLNLAIPIVVFTET			ļ	AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD
CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKÇIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDPEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET			1	VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS
RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKÇIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET	}			TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH
ITQAQEQQIELLEIPEHSDIKÇIAQPGAAYFYVELDTGEKLFHR IKKNFPLOFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDPEPYDFTLDD 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET				CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL
IKKNFPLOFGREVLASEAILNVFDKSDWRQCQISKEDEETLARR FRKDPEPYDFTLDD 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET				RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF
FRKDFEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNHFLNLAIPIVVFTET	i l			ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR
6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET		!	1	· · · · · · · · · · · · · · · · · · ·
VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET				· · · · · · · · · · · · · · · · · · ·
6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET	6905	1	226	· · · · · · · · · · · · · · · · · · ·
ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET				
	6906	3	611	
				1
				TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE
PTMVVQGVKMLYVPVMPGHAKKLKLTMHKLVKPTTEKKYVDLTV	{			· ·
SFAPDIDGDEDLPGPPVRYYFSHDTD				
6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS	6907	2	2228	
SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS				I "
DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT				
GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQOSS				II .
SSRLRSAVSRAGSLLWMVATSPGRLFRLLYNWAGTTWYRLTTAA				
SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ				_
TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL				
ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED)			
TLALLEGIVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE				- · · · · · · · · · · · · · · · · · · ·
DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE				DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE
DQLAGLQQELAALALKQSSVAEEVGLLFQQIQAVRDDVESQFFA				
WISQFLARGGGGRVGLLQREEMOAQLRELESKILTHVAEMQGKS		i	1	I WISOFLARGGGRUGILORFEMOAOLRFLESKILTHVAEMOCKS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
· ID	peginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptochan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i ———	sequence		\≈possible nucleotide insertion)
!	ļ		AREAAASLSLTLQKEGVIGVTEEOVHHIVKQALQRYSEDRIGLA
	j		DYALESGGASVISTRCSETYETKTALLSLFGIPLWYHSQSPRVI
	}		LQPDVHPGNCWAFQGPQGFAVVRLSARIRPTAVTLEHVPKALSP
			NSTISSAPKDFAIFGFDEDLQQEGTLLGKFTYDQDGEPIQTFHF
	_		QAPTMATYCVVELRILTNWGHPEYTCIYRFRVHGEPAH
6908	3	780	QVPSAAWLMAVCGLGSRLGLGSRLGLQGCFGAARLLYPRFQSRG
			POGVEDGDRPQPSSKTPRIPKIYTKTGDKGFSSTFTGERRPKDD
			QVFEAVGTTDELSSAIGFALELVTEKGHTFAEELQKIQCTLQDV
			GSALATPCSSAREAHLKYTTFKAGPILELEQWIDKYTSQLPPLT
			AFILPSGGKISSALHFCRAVCRRAERRVVPLVQMGETDANVAKF
			LNRLSDYLFTLARYAAMKEGNQEKIYKKNDPSAESEGL
6909	3	405	GRLLAVGTDLYGQRSSAPEQELLVQDATPVSNSLLPEKAFSDIP
]		SPYLRGT1KMMQAVRQAFQDQDDRRTWDGRPLTMAATFDDCLYA
	İ		LCVVDTIKESSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS
:			LYC
6910	1	1068	LVPVVVIDSYYYGKLVIAPLNIVLYNIFTPHGPDLYGTEPWYFY
:	!	j	LINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVQNLGHPYWLT
•	į		LAPMYIWF] FFIQPHKEERFLFPVYPLICLCGAVALSALQHSF
		ĺ	LYFQKCYHFVFQRYRLEHYTVTSNWLALGTVFLFGLLSFSRSVA
			LFRGYHGFLDLYPEFYRIATDPT1HTVPEGRPVNVCVGKEWYRF
			PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ
	1		NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY
:	1		RPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPRKAKQIRK
6911	1184	96€	KSGG
6911	1184	366	GEDAEEMETGNVANLISIFGSSFSGLLRKSPGGGREEEEGEESG
6912	1	844	PEAAEPGQICCDKPVLRDMNPWSTAIVAF AMKPVETHSFOMLFTILSTGSALKAQSYEDAYRCIKSSILLGSI
0512	. *	044	SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAVW
į	Ĭ	1	GESGELVCTKPIPCQPTHFWNDENGNKYRKAYFSKFPGIWAHGD
1			YCRINPKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFEEVE
ı			DSLCVPQYNKYREERVILFLKMASGHAFQPDLVKRIRDAIRMGL
			SARHVPSLILETKGIPYTLNGKKVEVAVKQIIAGKAVEQGGAFS
			NPETLDLYRDIPELOGF
6913	1643	. 1558	KKSHEESHKEELSYGAQASLPLPCSDFR
6914	1251	615	ELAAECKSAGYPGTLIPYRCDLSNEEDILSMFSAIRSOHSGVDI
			CINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTREAYQSMK
1			ERNVDDGHI ININSMSGHRVLPLSVTHFYSATKYAVTALTEGLR
*	1		QELREAQTH1RATCISPGVVETQFAFKLHDKDPEKAAATYEQMK
	1	•	CLKPEDVAEAVIYVLSTPAHIOIGDIQMRPTEQVT
6915	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6916	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
	1	1	ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
i	1	ł	VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6917	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
-			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
i]		VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6918	28	921	PEAGTRSWREPDPEDLRRFLLSAACRSFPQWLPGGGGGQVSSCS
			DTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSP
*		ł	VGEAGPDLUSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAW
			LGRHCPTVSFVLRAODDAFVHTPALLAHLRALPPASARSLYLGE
	į		VFTQAMPLKKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPW
	1		LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRT
:			ADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC
L	1	1	I : The same of th

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SEQ	Predicted	Fredicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanino, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1		amino acid	P=Proline, O=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	eeaneuce	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6919	850	41	QGRRELSGSVI CPFIQQEPKEMLTLSEYHERVRSQGQQLQQLQA
1		:	ELDKLHKEVS: "VRAANSERVAKLVFQRLNEDFVRKPDYALSSVG
į	i		ASIDLQKTSHT YADRNTAYFWNRFSFWNYARPPTVILEPHVFPG
{			NCWAFEGDQGQVVIQLPGRVQLSDITLQHPPPSVEHTGGANSAP
1			RDFAVFFLLSFFTHQGLQVYDETEVSLGKFTFDVEKSEIQTFHL
•		İ	QNDPPAAFPKVKIQILSNWGHPRFTCLYRVRAHGVRTSEGAEGS
ļ		<u> </u>	AQGPH
6920	1418	591	EAQGPSKVHL1 LKKKK
6921	2	1711	MNATRSEEQFEVINHAEQTLRKMENYLKEKQLCDVLLIAGHLRI
į			PAHRLVLSAVE DYFAAMFTNDVLEAKQEEVRMEGVDPNALNSLV
	1		QYAYTGVLQLKEDTIESLLAAACLLQLTQVIDVCSNFLIKQLHP
1		1	SNCLGIRSFGDAQGCTELLNVAHKYTMEHFIEVIKNQEFLLLPA
i	į		NEISKLLCSDTINVPDEETIFHALMQWVGHDVQNRQGELGMLLS
1	1		YIRLPLLPPQ:_ADLETSSMFTGDLECQKLLMEAMKYHLLPERR
1			SMMQSPRTKPKKSTVGALYAVGGMDAMKGTTTIEKYDLRTNSWL
1			HIGTMNGRRLCFGVAVIDNKLYVVGGRDGLKTLNTVECFNPVGK
1			IWTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTVERWDP
1	· ·	i	EGRQWNYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY
]		FDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHC
	ļ		SRLSDCVERYLPKGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG
	}		YDGHTYLNTVPSYDAQRNEWKEEVPVNIGRAGACVVVVKLP
6922	1075	365	LTPPAGIRHEVEDREREREREREREKEPLDSTGSELKQNIHSIT
	1		GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGGSTINDVLA
ļ			VNTPKDAAQQUAKAEENKKEPLCRQKQHRKVLDKGKPEDVMPSV
j	}		KGAQERLPTVILSGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK
			LPMGSIKNVVSEPIEGHEDYHMMAFQLGPTEASYYWVYWVPTQY
		<u> </u>	VDAI KDTVLGKWQYF
6923	2469	1660	LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ
ł	l		LPVTFGNKQKVlGKALSLIRFPLMTIEEFAAGPAQSGILSDREV
	1		VNLFLHFTVNFEPRVEYIDRPRCCLRGKECCINRFQQVESRWGY
İ		1	SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYEKK
			QTLGQNDTGF5 CDGTANTFRVMFKEP1E1LPNVCYTACATLKGP
		ì	DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP
			EIIFYT
6924	2210	1235	PEERVICFVEY? LTAFHEGRKGALAKKPYNPI IGETFHCSWEVP
	i	İ	KDRVKPKRTASHSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP
	Į.		ISCFYCECEEK&LCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE
			HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF
1	1	1	HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG
	1		ETKVIDTTTLEVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI
			DAATEQKRHLIEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ
			SPLESTLMGLEVOSFPV
6925	2	1653	RGGAAGAAMEF. SVIEDKTIELMCSVPRSLWLGCANLVESMCAL
		1	SCLQSMPSVRCDQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF
		i	DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP
			EQGLDHIAEN] SYLDARSLCAAELVCKEWQRVISEGMLWKKLI
			ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI
İ			IQDIETIESNW: CGRHNLQRIQCRSENSKGVYCLQYDDEKIISG
			LRDNSIKIWDK: SLECLKVLTGHTGSVLCLQYDERVIVTGSSDS
			TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV
			WDMASATDITLERVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW
1	1		STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC
			GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP
			RAPASTLCLRT1 VEHSGRVFRLQFDEFQIISSSHDDTILIWDFL
			NVPPSAQNETRSPSRTYTYISR
6926	1	733	SGRVAMDGLGLCFPEOGFPAGPPLLPPHMGGHYRDCQSLGAPPL

	T		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=bysine,
Į.	corresponding	to first	L=beucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
{	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	seanence	Codon, /=possible nucleotide deletion,
L	secuence		\=possible nucleotide insertion)
ł			DGYPLPTPDTSPLDGVDPDPAFFAAPMPGDCPAAGTYSYAQVSD
}			YAGPPEPFAGPMHPRLGPEPAGPSIPGLLAPPSALHVYYGAMGS
1	1		PGAGGGRGFOMQPOHOHOHOHOHHPPGPGQPTPPPEALPCRDGT
ì			DPSQPAELLGEVDRTEFEQYLHFVCKPEMGLPYQGHDSGVNLPD
	f	1	SHGAISSVVSDASSAVYYCNYPDV
6927	2	1484	LTLCGDICLMLAONANNRAAHLEEFHYQTKEDQEILESLHRESS
1			COGFAWATDLSTDLESQLSVSCKCYEAANEILQFRDLKSQNPEH
ì '			YVOVLKRMONIRNEIGVFYMNQAAALQSERLVSKSVSAAEQQLW
1)		KKSFSCFEKGIHNFESIEDATNAALLLCNTGRLMRICAQAHCGA
	i	}	GDE1, KREFSPEEGLYYNKAIDYYLKALRSLGTRDIHFAVWDSVN
1])	WELSTTYFTMATLQQDYAPLSRKAQEQIEKEVSEAMMKSLKYCD
1)		VDSVSARGFLCQYRAATIHHRLASMYHSCLRNQVGDEHLRKQHR
	Ì		VLADLHYSKAAKLFQLLKDAPCELLRVQLERVAFAEFQMTSQNS
}]	į .	NVGKLKTLSGALDIMVRTEHAFQLIQKELIEEFGQPKSGDAAAA
]	1		ADASPSLNREEVMKLLSIFESRLSFLLLQSIKLLSSTKKKTSNN
1			IEDDTILKTNKHIYSOLLRATANKTATLLERINVIVHLLGQLAA
1]		GSAASSNAVO
6928	1086	777	EAIDLINNLLOVKMRKRYSVDKTLSHPWLGDYOTWLDLRELECK
			IGERYITHESDDLRWEKYAGEQGLQYPTHLINPSASHSDTPETE
į	ļ	Į	ETEMKALGERVSIL
6929	1749	607	RDORGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG
			NLHOHDPODLRHNGNVVVAGRPSCSRGPRRAIQKPOPAGGRRSG
ł			RGPAAGGLCLOPPDGGTCVPEEPPVPPMDWEALEKHLAGLOFRE
	ļ		OEVRNOGOARTNSTSAOKNERESIROKLALGSFFDDGPGIYTSC
}			SKSGKPSLSSRLQSGMNLQICFVNDSGSDKDSDADDSKTETSLD
ł			TPLSPMSKQSSSYSDRDTTEEESESLDDMDFLTRQKKLQAEAKM
,			ALAMAKPMAKMOVEVEKONRKKSPVADLLPHMPHISECLMKRSL
ļ			KPTDLRDMT1GQLQVIVNDLHSQIESLNEELVQLLL1RDELHTE
ł			QDAMLVDIEDLTRHAESQQKHMAEKMPAK
6930	131	545	FKDTANVFVSLFOMRNNFRHYFIEPSQLKLFYDVITWIVTQVAI
1	}	1 2 2 2	SYTVVPFVLLSIKPSLTFYSSWYYCLHILGILVLLLLPVKKTQR
1	Í		RKNTHENIQLSOSKKFDEGENSLGQNSFSTTNNVCNQNQEIASR
1			HSSLKO
6931	2	659	FVERLPNRFACLLVASGAAEGVSAQSFLHCFTMASTAFNLQVAT
1	1		PGGKAMEFVDVTESNARWVODFRLKAYASPAKLESIDGARYHAL
j	i		LIPSCPGALTDLASSGSLARILOHFHSESKPICAVGHGVAALCC
1	}		ATNEDRSWVFDSYSLTGPSVCELVRAPGFARLPLVVEDFVKDSG
]	ì	1	ACFSASEPDAVHVVLDRHLVTGQNASSTVPAVQNLLFLCGSRK
6932	2	1131	FVDSPGOGEQAEEEEGGIOMNSRMRAHSPAEGASVESSSPGPKK
1 335	1 '	1	SDMCEGCRSLAAGEPGYISHDKETSIKYVSHQHPSHPQLFSIVR
]	1		OACVRSLSCEVCPGREGPIFFGDEOHGFVFSHTFFIKDSLARGF
1	1	ļ	ORWYSITTIMMDRIYLINSWPFLLGKVRGIIDELOGKALKVFEA
İ	1	1	
l	l		EQFGCPQRACRMNTAFTPFLHQRIGNAARSLTSLTSDDNLWACL
1]	1	HTSFAWLLKACGSRLTEKLLEGAPTEDTLVQMEKLADLEEESES
1	ĺ	ļ	WDNSEAEEEEKAPVLPESTEGRELTQGPAESSSLSGCGSWQPRK
!		,	LPVFKSLRHMRQVGGRGTAHHELRRRANHGLCLPTRLASGPSTL
	 	ļ	KTLQEVTDSLLGGWLMAQGVGGII
6933	1431	890	SLNLHCTLPF PPHQYPAGYPSDKEGKKPKGOSKKQPSGTTKRP1
1	1		SDDDCPSASKVYKASDSAEAIEAFQLTPQQQHLIREDCQNQKLW
}	1		DEVLSHLVEGPNFLKKLEQSFMCVCCQELVYQPVTTECFHNVCK
}	}	ļ	DCLORSFKAOVFSCPACRHDLGQNYIMIPNEILQTLLDLFFFGY
ł		<u> </u>	SKGR
	3030	2588	DRDHSQCGG!RRVALARVSSVKLISKAKIRTVKMTFIIVLAFIV
6934	} 3030	1 2224	
6934	3030		CWTPFFFVOMWSVWDANAPKEASAFIIVMLLASLNSCCNPWIYM
6934	3030		

SEO	Predicted	Predicted end	Amino acid secment containing signal pertide
פנ	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NC:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	lccation	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptopnan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	1	\=possible nucleotide insertion)
€535	886	543	NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMN1RRSTHDL
			VAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS
ı	İ		VGVAVLELLNFPPPSSPTLSVSSTSL
6936	1347	567	ESHRROFLSRALLEFFGKSHPPPHRLFRKSLNVGLHYSH1PFLT
0,550	. 2017	1	TCLHFLRKRLOKGEVGLSVETSKPOVPVGGLSRKKVPQEPWATV
1		1	MEKRLOEAOLYKEEGNORYREGKYRDAVSRYHRALLOLRGLDPS
Ī		1	LPSPLPNLGPOGPALTPEQENILHTTOTDCYNNLAACLLOMEPV
			NYERVREYSOKVLEROPDNAKALYRAGVAFFHLODYDOARHYLL
1	1		AAVNRQPKDANVRRYLOLTQSELSSYERKEKQLYLGMFG
€937	1	727	AVEFRCCPGRDPACFARGWRLDRVYGTCFCDOACRFTGDCCFDY
""	1	1 ""	DRACPARPCFVGEWSPWSGCADOCKPTTRVRRRSVQQEPONGGA
1			PCPPLEERAGCLEYSTPOGODCGHTYVPAFITTSAFNKERTRQA
			TSPHWSTHTEDAGYCMEFKTESLTPHCALENRPLTRWMOYLREG
			YTVCVDCOPPAMNSVSLRCSGDGLDSDGNOTLHWQAIGNPRCOG
1	1	İ	TWKKVRRVDQCSCPAVHSFIFI
6938	3	719	NSRKLELAERVOTDFMQLKKRRQSSEKENDSGTLDTVGAVVVDH
6536	,	,,,,	EGNVAAAVSSGGLALKHPGRVGQAALYGCGCWAENTGAHNPYST
			AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMONKFISS
			PFLASEDGVLGGVIVLRSCRCSAEPDSSQNKQTLLVEFLWSHTT
İ			ESMCVGYMSAODGKAKTHISRLPPGAVAGQSVAIEGGVCRLGEP
ł	1		SELTLOAECEASORHERT
6539	3	810	KVTAPRRPORYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS
0939		010	GYESLERDSEATGSASSAPDSMSESGAASPGARTTSLKSPKKRA
ĺ	1		TGLORRELI PAPLEDTTALGREPSLPGQWVDLPPPLAGSLKEPF
			EIKVYEIDDVERLORPRPTPREAPTQGLACVSTRLRLAERRQQR
1			LREVOAKHKHLCEELAETQGRLMLEPGRWLEQFEVDPELEPESA
Į.			EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAI PGPQ
1			EVDV
6940	1188	496	GKMAAOPLRHRSRCATPPRGDFCGGTERAIDOASFTTSMEWDTQ
1			VVKGSSPLGPAGLGAEEPAAGPOLPSWLQPERCAVFQCAQCHAV
1			LADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGS
			TYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLL
1			KTKAIVNASEMDIONVPLSEKIAELKEKIVLTHNRLKSLMKILS
			EVTPDOSKPEN
6941	 	713 :	SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEAQRQAEALGYQA
	_		VVLSAAMOGDVKSMAOFYGLLAHVARTRLTPSMAGASVEEDAQL
1			HELAAELOIPDLOLEEALETMAWGRGPVCLLAGGEPTVQLOGSG
ı			RGGRNOELALRYGAELRRWPLGPIDVLFLSGGTDGQDGPTEAAG
1	1	}	AWYTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGGAHLLHTG
I	1		MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG
1	_		CTYLNTMESYDPQTNEWTQMASLNIGRAGACVVVIKQP
6943	1	739	PMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLG
	1		HSPAGGSITETLYQGDKTEYLLTALEPKPTY11CMVTMETTNAY
			VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAG: IGGA
			VALVFLFLVLGAICWYVHOAGELLTRERAYNRGSRKKDDYHESG
1	1		TKKDNSILEIRGPGLOMLPINPYRAKEEYVVHTIFPSNGSSLCK
1	1		ATHTIGYGTTRGYRDGGIPDIDYSYT
6944	960	156	VANILLNGVKYESELTGSSERAEQPLSVGRLCSTICNMPKALRT
1]	1	LCVNHFLGWLSFEGMLLFYTDFMGEVVFQGDPKAPHTSEAYQKY
1			NEGVIMGCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYLA
1			FCLGTGLATLSRNLYVVLSLCITYGILFSTLCTLPYSLLCDYYQ
1			SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVLGPLTSA
	i		VCSANGVMYFSSLVSFLGCLYSSLFVIYEIPPSDAADEEHRPLL
	1	1	1
	1	<u>i</u>	LNV

	/ for 3:		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
\	amino acid	sequence	Codon, /=possible nucleotide deletion,
[sequence		\=possible nucleotide insertion)
6945	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAOGC
1	!		HSKPGPARPVPLKKRGYDVTRNPHLNKGMAFTLEERLQLGIHGL
			IPPCFLSQDVQLLRIMRYYERQQSDLDKYIILMTLQDRNEKLFY
1			RVLTSDVEKFMPIVYTPTVGLACQHYGLTFRRPRGLFITIHDKG
İ			HLATMLNSWPEDNIKAVVVTDGERILGLGDLGCYGMGIPVGKLA
	1		LYTACGGVNPOOCLPVLLDVGTNNEELLRDPLYIGLKHORVHGK
ł]		AYDDLLDEFMOAVTDKFGINCLIQFEDFANANAFRLLNKYRNKY
1	}		CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFQGAGEAAM
			G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH
	1]	LNHEKEMFAQD\HPEVNSLEEVVRLVKPTAIIGVAAIAEA\FTE
			QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF
1			FAS\GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWQLGVHSPG
			GDPGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR
1]	\	NVFLRIAIKVFD*GYKHNLV\SYYPEPKD\KEAFCKIPGSYTPD
l	i	1	YDSFYT/VDSYIWAQGKAMNVQTV
6946	133	2551	SCEYSGITVAPGDPCPGVAHLLAPSMASDTPESLMALCTDFCLR
1 0,720	133	22,52	NLDGTLGYLLDKETLRLHPDIFLPSEI\CDRLVNEYVELVNAAC
ļ			NF\EPHE\SFFNPLFRDPRKQPASRRIHL\RED\LVQD\QD\LE
1			AIRKQDL\VEL\YLTN\CEKLSAKSLQTLRSFSHTLGVP+AFFG
<u> </u>			C\TNILLLRKENPGGL/CEDEYLFNPTCQVLVKDFTFEGFSRLR
i		ļ	F\LKLGRMIDWYPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ
]	1	1	WKDSL\VSLVL\YNMDLSDDIIR\VIVQLHKLRHLDISRDRLSS
i	1	1	YYKFKLTREVLSLFVOKLGNLMSLDISG\HMILENCSISKIGKR
Į	ì		EAGQTSI\EPSK\SSIIPFRGFEGGPLQF\LGVF*GIFCGRLTH
1			IPAYKVSGDKNEEQVLNAIEAYTEHRPEITSRAINLLFDIARIE
	}	\	RCNOLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSEYRSE
ł			OSVKLRROVIOVVLNGMESYOEVTVQRNCCLTLCNFSIPEELEF
Ì	Ì		OYRRVNELLLSILNPTRODESIORIAVHLCNALVCOVDNDHKEA
ł			VGKMGFVVTMLKLTQKKLLDKTCDQVMEFSW\SALWNITDETPD
1	ĺ		NCEMFLNFNGMKLFLDCLNEFPEKQELHRNMLGLLGNVAEVKEL
1			RPOLMTSOFISVFSNLLESKADGIEVSYNACGVLSHIMFDGPEA
1	}	į.	WGVCEPOREEVEERMWAAIQSWDINSRRNINYRSFEPILRLLPQ
į			GISPVSCHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM
	1	}	l .
6947	ļ	1682	ATARQETKEMARKVIEHCSNFKEENMDTSR TSVSTIPRGLASARPOSRSWRCCPVWRRSPGRARGRGLKMLNVP
034/	2	1087	
}	1	1	SQSFPAPRSQQRVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG
}	1	l	LKGRLIEVTEEELKKHNKKDDCWICIRGFVYNVSPYMEYHPGGE
	1	l	DELMRAAGSDGTELFDQVHRWVNYESMLKECLVGRMAIKPAVLK
	1		DYREEEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFQTDSLVTI
1	!		/EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLISYTYW/R*A
	1		MRFRKIFLCGL/CESVGKIEIVLQKKENTSWDFLGHPLKNHNSL
		!	IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLQVPIGQ
ļ	i	[HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPNNKYIYFLIK
	1		IYPTGLFTPELDRLQIGDFVSVSSPEGNFKISKFQELEDLFLLA
}	i		AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSQLE
			KLAPKDKRLDVEFVLSAFISEWNGKQGHISPALLSEFLKRNLDK
			SKVLVC1CGPVPFTEQGVRLLHDLNFSKNE1HSFTA
6948	104	58	PDGAHSFFPDEYFTCSSLCLSCGVGCKKSMNHGKEGVPHEAKSR
	\$		CRYSHQYDNRVYTCKACYERGEEVSVVPXTSASTDSPWMGLAKY
			AWSGYVIECPNCGVVYRSRQYWFGNQDPVDTVVRTEIVHVWPGT
1	1	1	DGFLKDNNNAAQRLLDGMNFMAQSVSELSLGPTKAVTSWLTDQI
1	1		APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDSCSSK
İ	1	Í	TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRRRT
1	}	1	OETVE
6949	152	4656	GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGGKIRTRRCH
1			QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVC
	<u> </u>	<u> </u>	<u> </u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nuclectide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	b=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
<u></u>	3cquence		
1	1		SCSTDTSEVPRWPENKEDHLVYADEESSNITDGRITPEPAVSNT
ł			EEPSTTSTAST\YPDVLTRVSLYRSHLNFSMLESPALHCQPSTS
}			SAFPIGSSGFSLVKEIKDSTSQHDDDNISTTSGFSSRASDKDIT
l	1		VSKNTSLPPLNSPEAERSHSLSOHTATSSKKPAFNLSAFGTLSP
ĺ	1		SLGNSSILKTSQLGDSPFYPGKTTYGGALLAVRQSKLRNTPYQA
l			PVRRQMKAKQLSAQSYGVTSSTARRILQSLEKMSSPLADAKRIP
			SIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPV
Į.	ĺ		SIATNRSVYFKPSLTPSGEFRKTNORIDKKCSTGYEKNMTPGQN
1	}		REQRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP
1			LEEEEMEGPVLPKISLFITSSSLFTFNFSSPEITTSSPSPINSS
	1		OALTNKVCMTSPSSTGSPMFKFSSFIVKSTEANVLPPSSIGFTF
			SVPVAKTAELSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC
			EGPFRPAEILKEGSVLDILKSPGFASPKIDSVAAQPTATSPVVY
1	i		TRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC
			QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT
1			WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET
į			MTASSSSCTVTTGTLGFGDKFKRFJGSWECSVCCVSNNAEDNKC
}			VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC
1			ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS
ŀ			SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP
1	ì		MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL
ŀ			SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR
}	1		VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA
1	İ		TKGGFSFGNVEPASLPSASVFVLGRTEEKOCEPVTSTSLVFGEG
1	}		KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE
ŀ			SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS
1	1		AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST
	}		SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG
]	Ì		ATTTSSSAGSSFVFGTGPSAPSASPAFGANCTPTFGQSQGASQP NPPGFGS1SSSTALFPTGSQPAPPTFGTVSSSSQPPVFGQQPSQ
			SAFGSGTTPNSSSAFOFGSSTTNFNFTNNSPSGVFTFGANSSTP
1	}		AASAQPSGSGFPFNQSPAAFTVGSNGKNVFSSSGTSFSGRKIK
1	•		TAVEREK
6950	2585	411	
3330	2365	311	PRFGSRSGLCRRAGERGAVRAGGLSRRTRAE*IMDELHYQDTDS DVPEQRDSKCKVKWTHEEDEOLRALVRQFGQQDWKFLASHFPNR
ì			TDOOCOYRWLRVLNPDLVKGPWTKEEDOKVIELVKKYGTKOWTL
		1	IAKHLKGRLGKOCRERWHNHLNPEVKKSCWTEEEDRIICEAHKV
1]		LGNRWAEIAKMLPGRTDNAVKNHWNSTIKRKVDTGGFLSESKDC
1	1		KPPVYLLLELEDKDGLQSAQPTEGQGSLLTNWPSVPPTIKEEEN
1			SEEELAAATTSKEOEPIGTDLDAVRTPEPLEEFPKREDQEGSPP
			ETSLPYKWVVEAANLLIPAVGSSLSEALDLIESDPDAWCDLSKF
1	ì ·	·	· .
1	1		DLPEEPSAEDSINNSLVQLQASHQQQVLPPRQPSA\LVPSVTEY RLDGHTISDLSRSSRGELIF1SPSTEVGGSGIGTPPSVLKRQRK
1	}		RRVALSPVTENSTSLSFLDSCNSLTFKSTPVKTLPFSPSOFLNF
1	1		WNKQDTLELESPSLTSTPVCSOKVVVTTPLHRDKTPLHOKHAAF
	1		
1			VTPDQKYSMDNTPHTPTPFKNALEKYGPLKFLPQTPHLEEDLKE
1)		VLRSEAGIELIIEDDIRPEKOKRKPGLRRSPIKKVRKSLALDIV
	1		DEDMKLMMSTLPKSLSLPTTAPSNSSSLTLSGIKEDNSLLNQGF
1			LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTVACGGTRDQLFMQE
(053			KARQLLGRLKPSHTSRTLILS
6951	1940	239	AGPDDTMKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESL
}]		QVLPSGTPFGTMVTAPHSSTRHTSVVMLTPNFDGPPSQAAAPMA
}	}		TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT
			TSSKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTRRPPRP
		İ	PGSSRKGAGNSSRPVPPAPGGHSRSKEGQRGRNPSSTPLGQKRP
	1		LGKIFQIYKGNFTGSVEPEPSTLTPRTPLWGYSSSPQPQTVAAT

	1 200 200 200 200 200 200 200 200 200 20	T = 3:	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotice	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location.	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
[amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u> </u>	\=possible nucleotide insertion)
\	į.	Į.	TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDA
İ			TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCYP\CT
)	}		SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTTPQAP
1	ł	}	THPSRVSESTISGAKEETVA\PSP*PTGCPVLSPQWYPQPQAIS
1		Į	STAWSPPGPGSLGQQGTSPMWPRGTNRSTEPPSA*ARWISFG*S
1			WPSACPSPP\LCPADGVLHEEEEEEDRQPGEQPEAYGNNTHHPGT
}	}		TFQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVP
		<u> </u>	∤ C
6952	658	304	PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE
[PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT
1	1	Ì	ASRQARGELRLCLTTAVRGTSPSVSPVCQSS
6953	1512	349	NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES
1	1	1	FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
		ł	PLLELCQCPLCQLDCGSREQLIAHVYQHTAAVVSAKSYM\CPVC
			GRALSSPGSLGRHLLIHSEDGRSNCAVCGARFTSHATFNSEKLF
{	<u> </u>	ļ	EVLNMESLPTVHNEGPSSAEGKDIAFSPFVYPAGILLVCNNCAA
1	1		YRKLLEAQTPSVRKWALRRQNEPLEVRLQRLERERTAKKSRRDN
ł			ETPEEREVRRMRDREAKRLORMOETDEORARRLORDREAMRLKR
}	}		AIETPEKRQARLIREREAKRLKRRLEKMDMMLRAQFGQDPSAMA
1	-	}	ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH
6954	819	1	PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAAQN
1			*PQR*RWTEGNSPQASAVATPGQGASPAAPRCTP*PSRRHRRLP
1	j		PGARPPAG*AAPAPTKPWLAGPASAPQPGAAPLSPPAPPLIRTR
	[*CAGAAARGRPRRDRSPRPRTPGGCSWSEPRTPPAVSASAOTPS
1	1	1	DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHRREGTIPGNPHPR
}		1	AS*RAGWQR*PGP/REWGL*EPQGEEMSGPGGPGGAFPNQVGSS
}	1		VMQAMSTGI
6955	196€	782	PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRTMPFLGQD
		ļ	WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSED
1		1	GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKESTK
}	ļ		ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLTS
ţ	1		LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCIL
			/N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\NG
i	i		LTLSDLPLHMLNNILYRFSDGWDIITLGQVTPTLYMLSEDRQLW
			KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQY
Į.		d.	GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLFK
			F
6956	8605	3839	QTSTS1FASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQSS
!	}	1	DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAAS
l	(PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTASV
			TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGEGLT
			ASGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRWQGETW
	1	İ	YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDFF
1	(EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKEV
1	1		PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAKI
	1		AKSKKKMRQKVORGECOTTIQGQARNKRKQETKSLKQKEAKKKS
			KAEKEKGKTKQEXLKEKVKREKKEKVKMKEKEEVTKAKPACKAD
	(KTLATORRLEEROROOMILEEMKKPTEDMCLTDHQPLPDFSRVP
1	}		GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEGL
			LCQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSEI
			PLTRDNVSEILRCFLMAYGVEPALCDRLRTOPFOAQPPQQKAAV
			LAFLVHELNGSTLIINEIDKTLESMSSYRKNKWIVEGRLRRLKT
			VLAKRTGRSEVEMEGPEECLGRRRSSRIMEVTSGMEEEEEESI
	1		AAVPGRRGRRDGEVDATASSIPELEROIEKLSKROLFFRKKLLH
			SSQMLRAVSLGQDRYRRRYWVLPYLAGIFVEGTEGNLVPEEVIK
			KETDSLKVAAHASLNPALFSMKMELAGSNTTASSPARARGRPRK
L	1		PETROPHARMOTHERMIT GERMINGSHIT INGGENEURGKERK

SEO	Predicted	Predicted end	Amino ació segment containing signal peptide
10	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	b=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	
1	sequence	seducince	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
j		!	TKPGSMQPRHLKSPVRGQDSEQPQACLQPEAQLHAPAQPQPQLQ
1		į	LQLQSHKGFLEQEGSPLSLGQSQHDLSQSAFLSWLSQTQSHSSL
1		ļ	LSSSVLTPDSSPGKLDPAPSQPPEEPEPDEAESSPDPQALWFNI
ı	<u> </u>		SAQMPCNAAPTPPPAVSEDQPTPSPQQLASSKPMNRPSAANPCS
1	}	į	PVQFSSTPLAGLAPKRRAGDPGEMPOSPTGLGQPKRRGRPPSKF
			FKQMEQRYLTQLTAQPVPPEMCSGWWWIRDPEMLDAMLKALHPR
1			GIREKALHKHLNKHRDFLQEVCLRPSADPIFEPRCLPAFQEGIM
J		}	SWSPKEKTYETDLAVLQWVEELEQRVIMSDLQIRGWTCPSPDST
1			REDLAYCEHLSDSQEDITWRGRGREGLAPQRKTTNPLDLAVMRL
1			AALEONVERRYLREPLWPTHEVVLEKALLSTPNGAPEGTTTEIS
1]	1	YEITPRIRVWROTLERCRSAAQVCLCLGQLERSIAWEKSVNKVT
[CLVCRKGDNDEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTV
			CLAQQVEGEFTQKPGFPKRGQKRKSGYSLNFSEGDGRRRRVLLR
			GRESPAAGPRYSEEGLSPSKRRRLSMRNHHSDLTFCEIILMEME
]]]	SHDAAWPFLEPVNPRLVSGYRRIIKNPMDFSTMRERLLRGGYTS
1			SEEFAADALLVFDNCQTFNEDDSEVGKAGHIMRRFFE\SRWEEF
1			YQGKQGCSVRQGRWGVTLWHLPPTFQTKTCHFHLLMLPWVQTQV
ļ			RYNPDF
6957	82	3514	ELIVAMPEPTKKEENEVPAPAPPPEEPSKEKEAGTTPAKDWTLV
ł			ETPPGEEQAKQNANSQLSILFIEKPQGGTVKVGEDITFIAKVKA
			EDLSEKPTINGSRKWMDLASKAGKHLQLKETFERESRVYTFEMQ
ļ	ļ		IIKAKDNFAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIR
1	1		SAFKRSGEGQEDAGELDFSGLLXRREVKQQEEEPQVDVWELLKN
1			TKPSEYEKIAFOYESPTCSGMLKRLKRSIREEKKSAAFAKILDP
			VYQVDKGGRVRFVVELADPKLEVKWNKNGQELRPSTKYIFEDTR
}		į	CQSILNIDNCOMTDDSEYYVTAGDEKCSTELLVREPPIMVTKQL
1			EDTTDYCGERVELECEVSEDDAQVKWFKNGEEIILVQTRYRIRV
{]	EGKKHILIIEGATKADAADYSVMTTGGQSSAKLSVDLKPLKILT
1			PLTDQTVNLGKEICLKCEISENIPGKWTKNGLPVQESDRLKVVH
			KGRIHKLVIDHALTEDEGDYVFAPDAYNVTLPAKVHVIDPPKII
\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \			LDGLDADNTVTVIAGNKLRLEIPISGEPPPKAMWSRGDKAIMEG
			SGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGEAHASIK
			VKVVDFPDPPVAPTVTEVGDDWCIMNWEPPAYDGGSPILGYFIE
į			RKKKQSSRWMRLNFDLCKETTFEPKKMIEGVAYEVRIFAVNA\I
}	1	}	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI
			GAAGLDGYVLEYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD
			LIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVKE
			IIEPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD
}			GAEIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE
	· ·		TASIDIRIIDRPGPPOIVKIEDVWGRNVALTWTPPKDDGNAAIT
			GYTIQKADKKSMEWLRVIEHIIEPVFHTELVIGNEYYFRVFSEN
		-	MCGLSEDATMTKESAVIARDGKIYKNPVYEDFDFSEAPMFTQPL
			VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS
			NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ
6958	274	1663	PRTSRVKTEGSOGSSAMDFSVKVDIEKEVTCPICLELLTEPLSL
			DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR
}			HLANIVERVKEVKMSPQEGQKRDVCEHHGKKLQIFCKEDGKVIC
			WVCELSQEHQGHQTFRINEVVKECQEKLQVALQRLIKENQEAEK
			LEDDIRQERTAWKNYIQIERQKILKGFNEMRVILDNEEQRELQK
			LEEGEVNVLDNLAAATDQLVQQRQDASTLISDLQRRLRGSSVEM
(LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVLKE
			LTDVQYYWVDVMLNPGSATSNVAISVDQRQVKTVRTCTFKNSNP
			CDFSAFGVFGCOYFSSGKYYWEVDVSGKIAWILGVHSKISSLNK
[RKSSGFAFDPSVNYSKVYSRYRPQYGYWVIGLQNTCEYNAFEDS
[SSSDPKVLTLFMAV\LPVVLGFS
6959	1	1469	SLVHVVEFGRGIEDFPYLFFQLTHCQQRICSVTQAGVQWCDHSS

SEQ	Fredicted	Predicted end	liming said segment containing signal portion
. ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l No:	location	corresponding	
ì		to first	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
}	1	1	P=Proline, Q=Glutamine, R≈Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stor
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotice insertion)
1	1		LOPOTPGLNQSSHLSLLSSRDYRMLSSFNEWFWQDRFWLPPNVT
<u> </u>			WTELEDRDGRVYPHPODLLAALPLALVLLAMRLAFERFIGLPLS
ì	}		RWLGVRDOTRRQVKPNATLEKHFLTEGHRPKEPOLSLLAAQCGL
}	\		TLQQTGRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSFVGGLSV
1			LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\S1YWWYLLELG
Į.	ļ		FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFKEQVIH
l	l	{	HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACKMVNYMC
1		i i	YQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESISNRGPFF
)	1		GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDIRSDV
}	Ì		EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTN
	ļ		RHTTAT
6960	387	2068	AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS
	l		HLEPEEKOALKRLVEEEPLKMQVDEAASREDKLDLTKKGKRPPT
1	Į.		PCSDPERKRFRFNSESESGSEASSPDYFGPPAKNGVASRSHTEF
ł			KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEEKGYKGK
	i		TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN
Ì	ì	1	KGTKSLKESEQESEEEILAQKKEQREEEVEEEEKEEDEEKGDWK
}			PRTRSNGRRKSAREERSCKOKSQAKRLLGDSDSEEEQKEAASSG
l		ļ	DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTA.
1	ţ		KGSRKMARLGSTSGEESDLEREVSDSEAGGGPOGERKNRSSKKS
((SRKGRTRSSSSSSDGSPEAKGGKAGSGRRGEDHFAVMRLKRYIR
l			ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCR
	ĺ		ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGE
			LYRRTLDSDEERPRFAPPDWSHMRGIISSDGESN
6961	340	1646	RPWSSPIMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
1		ĺ	NOESFOLALLEEVWSEODFQYLRQKLSPTYPAAHHFRSGIIGSG
1			LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
}	}		SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELACFIHHTSKK
ļ	!		ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
ţ			NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
l		į	TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
i .	1		PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
			LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
6962	340	1646	LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGCQEGDRTKEQ
0.762	340	1046	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
	f		NQESPOLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
			LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
٠.	ļ		SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
	1		NTMVPKNCYVSQOELKPFPFGVRIDYVLYKAVSGFYISCKSFET
	1		TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
			1
			PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
	1		
6963	374	2610	LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
0263	3/4	2618	RVTPLILKLLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF
Į I	l		EAVLSPDPALIESTHSLTNSHAHTGSSDCDISCKGMTERIESIN
	Į.		LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS
	}		PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA
]		LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG
	1		TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE
	}	}	RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL
			STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ
			ILERNESEECTEDTDOAEGTESEPKGESFDSGVSSSIGTEPDSV
			·-
			EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNOLETGASSPE
			·-

WO 01/53312 PCT/US00/34263

Deginming nuclectide location corresponding to first amino acid residue of anino acid residue of anino acid anino acid sequence properties anino acid sequence sequence sequence properties anino acid anino acid sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Note Incention Corresponding Correspon	i -			
corresponding	1			
to first amino acid residue of amino acid aequence Sequ	1 10.	i	<u> </u>	1
to first amino acid residue of amino acid residue of amino acid sequence #TYPYCOPHAN, Y-TYYROSHAN, X-UNROWN, *-Stop Codon, /-possible nucleotide deletion, Y-possible nucleotide deletion, Y-possible nucleotide deletion, Y-possible nucleotide deletion, Y-possible nucleotide insertion) ### PFIFEERPFIRAGOTPOTYVORGHCYPYTOTYCHENGESTAGGER CORRESTEDED, MAGOTOTYVORGHCYWITGERUPICOSI CRRSTELEDPIRAGOTPOTYVORGHCYWITGERUPICOLIUS CRRSTELEDPIRAGOTPOTYVORGHCYWITGERUPICOLIUS CRRSTELEDPIRAGOTPOTYVORG				· · · · · · · · · · · · · · · · · · ·
amino acid residue of amino acid sequence	1			
residue of amino acid sequence Sequence	:	li .	5	
amino acid sequence Codom, /=possible nucleotide deletion, /=possible nucleotide insertion) PFIFELPOFILAGOTOFYTYSOPGISTFTAGIA-PAPOFIASSAGH PFIFELSOFILLOW THE TAKON VIMEN-WITESCHEPHOCS I CHRS PSILAGULIAN FT TAKON VIMEN-WITESCHEPHOCS I CHRS PSILAGULIAN FT TAKON VIMEN-WITESCHEPHOCS I CHRS PSILAGULIAN FT TAKON VIMEN-WITESCHEPHOCS I CHRS PSILAGULIAN FT TAKON VIMEN-WITESCHEPHOCS I CHRS PSILAGULIAN FTO CHRS PSI	1		1	l · · · · · · · · · · · · · · · · · · ·
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6969 1855 118 AGTMHGRLKVKTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQA GELDESVLELTSQILGANPDFATLWNCRREVLQQLETQKSPEEL AALVKAELGFLESCLRVNPKSYGTWHHRCWLLGRLPEPNWTREL ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFTDSLITR NFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPEDVLLKELELVQN AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSTEDACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKBLQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLINLQGNPLCQAVGILEQLAELL	1	1	}	
GELDESVLELTSQILGANPDFATLWNCRREVLQQLETQKSPEEL AALVKAELGFLESCLRVNPKSYGTWHHRCWLLGRLPEPNWTREL ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFTDSLITR NFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPEDVLLKELELVQN AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKBLQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEQLAELL				
AALVKAELGFLESCLRVNPKSYGTWHHRCWLLGRLPEPNWTREL ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFTDSLITR NFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPEDVLLKELELVQN AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKELQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEOLAELL	6969	1855	118	
ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFTDSLITR NFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPEDVLLKELELVQN AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKBLQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEOLAELL		1		
NFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPEDVLLKELELVQN AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFFCELSVEKSTVLQSELESCKBLQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEOLAELL	1		i	
AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCROSTTDE QLFRCELSVEKSTVLQSELESCKBLQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLBQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEOLAELL			1	I .
SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKBLQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLINLQGNPLCQAVGILEOLAELL	}	}	ì	
AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKBLQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLINLQGNPLCQAVGILEOLAELL		1 .	1	
QLFRCELSVEKSTVLQSELESCKBLQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLINLQGNPLCQAVGILEQLAELL		1		
RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLINLQGNPLCQAVGILEQLAELL	1	}		1
VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLINLQGNPLCQAVGILEQLAELL		Į.		
PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEOLAELL	1	1		
CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEQLAELL			Į.	
			1	
PSVSSVLT	1	J	J	
		<u> </u>		PSVSSVLT

			13
SEQ	Precieted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotice	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 1	corresponding	to first	b=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 1	sequence	_	\=possible nucleotide insertion)
6970	3	1528	SFPPLLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIQLEPLNE
			GFLSRISGLLLCRWTCRHCCQKCYESSCCQSSEDEVEILGPFPA
1			OTPPWLMASRSSDKDGDSVHTASEVPLTPRTNSPDGRRSSSDTS
i i			KSTYSLTREISSLESRRPSSPLIDIKPIEFGVLSAKKEPIOPSV
		1	LERTYNPDDYFRKFEPHLYSLDSNSDDVDSLTDEEILSKYQLGM
1 1			LIFSTOYDLLHNHLTVRVIEARDLPPPISHDGSRQDMAHSNPYV
1 1		1	K3CLLPDOKNSKOTGVKRKTOKPVFEERYTFEIPFLEAQRRTLL
1 1		i	LTVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHWWKALIPSSQNE
1		}	VELGELLLSLNYLPSAGRLNVDVIRAKOLLQTDVSQGSDPFVKI
			CLVHGLKLVKTKKTSFLRGTIDPFYNESFSFKVPQEELENASLV
1			FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRMLNTHRT
		į	EVEOWHSLRSRAECDRVSPASLEVT
	 	3702	ACFYVPGSRSFKLIPRHGLVNMGRSGKLPSGVSAKLKRWKKGHS
6971	37	3 /02	•
1		l	SDSNPAICRHRQAARSRFFSRPSGRSDLTVDAVKLHNELQSGSL
1	}	}	RLGKSEAPETPMEEEAELVLTEKSSGTFLSGLSDCTNVTFSKVQ
1			RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEYFAALIRKA
}		}	ACHGVCSVLKGSEFMFEKAPAHHPAAISTAKFCIQEIEKSGGSK
}		1	EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA
1 .		į	CAMQAFHSLFHARPGLSTLSAELNAQIITALYDYVPSENDLQPL
	Į	ĺ	LAWLKVMEKAHINLVRLQWDLGLGHLPRFFGTAVTCLLSPHSQV
1 :			LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV
		•	EEGLTYKFHAAWSSVLQLLCVFFEACGROAHPVMRKCLQSLCDL
1	}	1	RLSPHFPHTAALDQAVGAAVTSMGPEVVLQAVPLEIDGSEETLD
1 '			FFRSWLLPVIRDHVQETRLGFFTTYFLPLANTLKSKAMDLAQAG
1			STVESKIYDTLQWQMWTLLPGFCTRPTDVAISFKGLARTLGMAI
i			SERPDLRVTVCQALRTLITKGCQAEADRAEVSRFAKNFLPILFN
}	}	}	LYGQPVAAGDTPAPRRAVLETIRTYLTITETQLVNSLLEKASEK
1			VLDPASSDFTRLSVLDLVVALAPCADEAAISKLYSTIRPYLESK
į		1	AHGVQKKAYRVLEEVCASPQGPGALFVQSHLEDLKKTLLDSLRS
(1	[TSSPAKRPRLKCLLHIVRKLSAEHKEFITALIPEVILCTKEVSV
1		ĺ	GARKNAFALLVEMGHAFLRFGSNQEEALQCYLVLIYPGLVGAVT
1	İ		MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLLASRTRDVV
1			KSALGFIKVAVTVMDVAHLAKHVQLVMEAIGKLSDDMRRHFRMK
1	1	1	LENLFT\KF1PK\FGILTWGKKAVGPKEYHRVLVN1RKAEARAK
		Ì	RHRALSQAAVEEEEEEEEEEPAQGKGDSIEEILADSEDEEDNE
}		1	EEERSRGKEORKLARQRSRAWLKEGGGDEPLNFLDPKVAQRVLA
1	}	j	TOFGPGRGRKKDHSFKVSADGRLIIREEADGNKMEEEEGAKGED
1	Í	1	EEMADPMEDVIIRNKKHQKLKHQKEAEEEELEIPPQYQAGGSGI
1	{	}	HRPVAKKAMPGAEYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNR
			RKKMKLOGQFKGLVKAAQRGSQVGHKNRRKDRRP
6972	2179	973	PGGATLLPLWRRTRPREATVPRGAAQRGRARSAEGRIPSSQSPS
1		l	PAEAGGATRSPPPRPPRPPRPARPPGPSAPPLLRSDAGPGATVSAAA
l		1	AAATERARRGATMGAQLSTLGHMVLFPVWFLYSLLMKLFQRSTP
1	1	1	AITLESPDIKYPLRLIDREIISHDTRRFRFALPSPQHILGLPVG
1			QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK
ì	1)	FPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKK
1		1	SNPIIRTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF
	1	1	ANOTEKDILLRPELEELRNKHSARFKLWYTLDRAPEAWDYGQG\
1		1	FVNEEMIRDHLPPPE/EEPLVLMCGPPPMIQYACLPNL/DHVGH
1		1	PTERCFVF
6973	1	1964	LOFRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA
1	ļ	1	SPRROEILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKQ
1		1	KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY
	[RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV
1	ì	l	KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL
1			
1		1	NVVGFPLNHFCKOLVKLYYPPRPEDLRRSVKHDSIPAADTFEDL

SEQ	Predicted	Predicted end	1 Aming haid commont containing charal nontide
ID	beginning	nuclectide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotice	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	b=Leucine, M=Methionine, N=Asparacine,
. 	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	resione of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	Beguerice	· · · · · · · · · · · · · · · · · · ·
	seduence	<u> </u>	\=possible nucleotide insertion; SDVEGGGSEPTORDAGSRDEKAFAGEAGOATAFAECHRTRETLP
1	İ	ĺ	
			PFPTRLLELIEGFMLSKGLLTACKLKVFDLLKDEAPQKAADIAS
ĺ			KVDASACGMERLLDICAAMGLLEKTEQGYSNTETANVYLASDGE
ł	l .		YSLHGFIMHNNDLTWNLFTYLEFAIREGTNOHHRALGKKAEDLF
1	1		ODAYYQSPETRLRFMRAMHGMTKLTACQVATAFNLSRFSSACDV
l	1		GGCTGALARELAREYPRMQVTVFDLPDIIELAAHFQPPGPQAVQ
			IHFAAGDFFRDPLPSAELYVLCRILHDWPDDKVHKLLSRVAESC
j	1		KPGAGLLLVETLLDEEKRVAQRALMQSLNMLVQTEGKERSLGEY
			OCLLELEGFHOVQVVHLGGVLDAIL\PPKWPPEAQAACSL
6974	3082	21.72	RSCAAFASFASRPPLELFAPPGSHRSPPGRGVATSAQCALSVRK
	1		LLAARPGLGTKYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV
	1		SLPTNIVPPTTIWTSSPONTDADTASFSNGTHNNSVLPVTASAP
	4		TSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVH
	1	}	LTTTLEEHSLGTPEAGVAATLSQSAAEPPTLISPOAPASSPSSL
1	1	Ì	STSPPEVFSASVTTNHSSTVTSTQPTGAPTAPESPTEESSSDHT
			! PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\PPPFPG
6975	2 .	500	RPRPTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKEL
1	1		KELLQTELSGFLDVKELML*ATEALKTFEEA*KSPIIQCSSSRS
1	j		SLPPAPQPPPYL*LSAVPFPIHLPLPLLPPQAQKDVDAVDKVMK
			ELDENGDGEVDFQEYVVLVAALTVACNNFFWENS
6976	1216	970	GCQL*VAYGTTENSPVTFAHPPEDTVEQKAESVGRIMPHTEARI
			MNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPOKTEBAVDQDKW
1	1	į	YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH
l		j	PKVQEVQVVGVKDDRMGEEICACIRLKDGEETTVEEIKAFCKGK
-			ISHFKIPKYIVFVTNYPLTISGKIQKFKLREOMERHLNL*IKQQ
			ACPGRLA
6977	1298	588	SLF1NTNLLSNQ1RKTSFGMCSEP1SDNTEDQKGKLKTPDFA*R
•			ANKKSKHHVNGNRTVEPFPEGTQMAVFGMGCFWGAERKFWVLKG
ł			VYSTOVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE
	l		ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS
1	1		KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQOYLSKNPNGY
			CGLGGTGVSCPVGIKK
6978	3	242	SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKCRLQQLFKGSQ
	<u> </u>		FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
6979	3917	1146	DEARVRGEAVAAAILSRCRHWSGPPPFPPSPPDRKGLRGTEPWE
	1		AGPGSGATPGARAMDVRRLKVNELREELQRRGLDTRGLKTELAE
			RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT
	1		AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE
1		!	NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP
			DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPOPPAEEDEDDFD
1	1		DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG
	1		VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL
ł			GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN
1			DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
			GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV
1]		GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR
1	j		NYAGRWDVL1QQATQCLNRL1Q1AARKKRNYTLDOTNVYGSAQR
	1		RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL
1	!		EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP
1			PPEKRFDNRGGGGFRGRGGGGGGFQRYENRGPFGGNRGGFQNRGG
	-		GSGGGGNYRGGFNRSGGGGYSONRWGNNNRDNNNSNNRGSYNRA
1			POOOPPPOOPPPOOPPPPPSYSPARNPPGASTYNKNSNI
1			PGSSANTSTPTVSSYSPPOSFGFFPSTFOPSYSOPPYNOGGYSO
			GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY
1			NOYCOYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTQGGTSTQ
6980	1	420	GTRGRKTGRVAAPSTRRRTGNMOKLQTRSPAMSLSDPGLGYHPT
	L		OTHORNEON AND STUDIO ST

No: nucleotide location nucleotide location location corresponding to first damino acid residue of residue of residue of amino acid sequence mino acid sequence mino acid sequence mino acid sequence mino acid sequence mino acid sequence mino acid mino acid sequence mino acid mino acid sequence mino acid mino acid sequence mino acid mino acid sequence mino acid mino acid sequence mino acid mino acid sequence mino acid mino acid mino acid mino acid mino acid sequence mino acid mino acid mino acid mino acid mino acid mino acid sequence mino acid mino a	ID	beginning nucleotide	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Clutamic Acid, E=Dhonylelanine, C=Cluster
No. nuclectide location corresponding to first amino acid to first amino acid residue of amino acid residue of amino acid sequence sequence maino acid sequence maino acid sequence corresponding to first leucine, M=Methionine, N=Asparagine, P=Polline, O=Glutamine, R=Arginine, S=Serie, T=Threonine, V=Aulnine, S=Stop Codon, /=possible nuclectide deletion, \possible nucleotide losertion) codon, /=possible nucleotide msertion) codon, /=possible nucleotide msertion codon, /=possi		nucleotide	1	Clutamic Acid Paphanulalanina Caclusina
corresponding corresponding corresponding corresponding corresponding corresponding corresponding cofirst amino acid residue of residue of amino acid residue of amino acid sequence Seserine, T=Threonine, V=Valine, N=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, N=Dossible nucleotide Codon, /=poss				
corresponding to first amino acid p=Proline, Q=Glutamine, R=Arginine, residue of amino acid amino acid amino acid sequence S=Serine, T=Threonine, V=Valine, Codon, /-possible nucleotide deletion, v=possible nucleotide insertion) CWTLRWPPLCSLHALHVHCLFSSRIGTPVSPRLAMDPNCSCE GSSCACAGSCKCKKCSCKSCSCPLGCAKCAGGCICKG SEKCSCCA SEKCSCCA PGSRFRASLRPAFAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFPAPAARGVPGGGLGGAXQARTRACAALPTPHP APRLLEPQGVFSLFFAARGVPGGGLGAXQARTRACAALPTPHP APRLLEPQGVFSLFFAARGVPGGGLGAXQARTRACAALPTPHP APRLLEPQGVFSLFFAARGVPGGGLGAXQARTRACAALPTPHP APRLLEPQGVFSLFFAARGVPGGGLGAXQARTRACAALPTPHP APRLLEPQGVFSLFFAARGVPGGGLGAXQARTRACAALPTPHP APRLLEPQGAARAVAALAAVAANATVLEDGAAAVAALAAVAAAVAAAAAAAAAAAAAAAAAAAAAAAA			corresponding	Halistidine Talsoleucine Valueine
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CREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQPYFKGI IFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLI GEGFILGGVFVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKM: KPQTLASEKK KPQTLASEKK GGRSAYSLPAGSLFRVPATAAAKMASGVQVADEVCRIFYDMKVI KCSTPEBIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTI: DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELJ PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLG GSLIVAFEGCPV RRTAGIYPCFPKPGRTRHALCSVVLLIJ.TGQLAFDDFQESCAMI WQKYAGSRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALI YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFYDIVDAKLI IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFI	6983	82	1773	
IFLDEKKKFYGPORRKMMFMGFIRLGVWYNFFRAWNGGFSGNLI GEGFILGGVFVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKM KPQTLASEKK 6984 1845 1282 GGRSAYSLPAGSLFRVPATAAAKMASGVQVADEVCRIFYDMKVI KCSTPEBIKKRKRAVIFCLSADKKCIIVEEGKEILVGDVGVTIT DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELL PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLG GSLIVAFEGCPV 6985 1887 1324 RRTAGIYPCFPKPGRTRHALCSVVLLILITGOLAFDDFQESCAMM WQKYAGSRRSMPLGARILFHCVFYAGGFAIVYYLIQKFHSRALY YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLM IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFI				· i
GEGFILGGVFVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKM. KPQTLASEKK 6984 1845 1282 GGRSAYSLPAGSLFRVPATAAAKMASGVQVADEVCRIFYDMKVI KCSTPEBIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELJ PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKK GSLIVAFEGCPV 6985 1887 1324 RRTAGIYPCFPKPGRTRHALCSVVLLIJTGOLAFDDFQESCAMM WQKYAGSRRSMPLGARILFHCVFYAGGFAIVYYLIQKFHSRALJ YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLM IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFM		1	i	
KPQTLASEKK 6984 1845 1282 GGRSÄYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVI KCSTPEBIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELJ PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLO GSLIVAFEGCPV 6985 1887 1324 RRTÄGIYPCFPKPGRTRHALCSVVLLLIJTGQLAFDDFQESCAM WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALJ YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLI IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFI				1
6984 1845 1282 GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVI KCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELJ PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLA GSLIVAFEGCPV 6985 1887 1324 RRTAGIYPCFPKPGRTRHALCSVVLLIJTGQLAFDDFQESCAMI WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALJ YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLI IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFI				
RCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELJ PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLG GSLIVAFEGCPV 6985 1887 1324 RRTAGIYPCFPKPGRTRHALCSVVLLIJ.TGQLAFDDFQESCAMN WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALY YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFYDIVDAKLG IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFI	6997	3045	1303	
DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELL PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLO GSLIVAFEGCPV 6985 1887 1324 RRTAGIYPCFPKPGRTRHALCSVVLLIJTGQLAFDDFQESCAM WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALY YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLI IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFI	0009	1045	1282	· }
PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLO GSLIVAFEGCPV 6985 1887 1324 RRTAGIYPCFPKPGRTRHALCSVVLLIJ.TGQLAFDDFQESCAM WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALY YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLI IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFI				
GSLIVAFEGCPV 6985 1887 1324 RRTAGIYPCFPKPGRTRHALCSVVLLIJ.TGQLAFDDFQESCAMN WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRAL) YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLN IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFN		1	ł	
6985 1887 1324 RRTAGIYPCFPKPGRTRHALCSVVLLLIJTGQLAFDDFQESCAM WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALY YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLH IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFF				1
WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRAL YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLI IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFI	6985	1887	1224	
YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLI IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFI	0,000	1007	1327	
IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFI		1		
1			Ì	
		1]	LSGENGDEVKKE
	6986	642	1350	YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQFDFKMYIAF
, and the second	0.500		1330	VFKEKKKKSALFEVSEVIPVMTNNYEENILKGVRDSSYSLESSL
1 1		1		ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC
)		1		LLFSRWKESDEPFRPVOAKFEFHHGDYEKOFLHVLSRKDKTGIV
				VNNPNQSVFLFIDRQHLQTPKNKATIFKLCSICLYLPQEQLTHW
AVGTIEDHLRPYMPE		1	1	· -
	6987	1623	341	LEAAEKASRAFKESQRQTDSKNYETENWSPOKSQRRYDMYNTAC
	050,	1323	1 234	FLGEIEVGLYTIQILQLTPFFHKENELSKKHMVQFLSGKWTIPP
		J		l ·
· · · · · · · · · · · · · · · · · · ·			i	DPRNECYLALSKFTSHLKNLQSDLKRCFDFFIDYMVLLKMRYTQ
, , , , , , , , , , , , , , , , , , , ,		1		KEIAEIMLSKKVSRCFRKYTELFCHLDPCJLQSKESQLLQEENC
<u> </u>		1		RKKLEALRADRFAGLLEYLNPNYKDATTMESIVNEYAFLLQQNS
				KKPMTNEKQNSILANIILSCLKPNSKLIQPLTTLKKQLREVLQF
1 "				VGLSHQYPGPYFLACLLFWPENQELDQDSKLIEKYVSSLNRSFR
1 1		Į.		GOYKRMCRSKQASTLFYLGKRKGLNSIVHKAKIEQYFDKAQNTN
		1		SLWHSGDVWKKNEVKDLLRRLTGQAEGKLISVEYGTEEKIKIPV
ISVYSGPLRSGRNIERVSFYLGFSIEGPPGL				ISVYSGPLRSGRNIERVSFYLGFSIEGPPGL
		<u> </u>		
1	6988	3	689	TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR
	6988	3	689	LVRGLGAASTAAPQDAQTGPQPMPRADCIMRHLPYFCRGQVVRG
KMVVSIGWNPYYKNTKKSMETHIMHTFKEDFYGEILNVAIVGYI	6988	3	689	LVRGLGAASTAAPQDAQTGPQPMPRADCIMRHLPYFCRGQVVRG FGRGSKQLGIPTANFPEQVVDNLPADISTGIYYGWASVGSGDVH

SEQ	Fredicted	Predicted end	Amino acid segment containing signal warrant
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, L=
NO:	nucleotide	location.	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŧ	corresponding	to first	L=Leucine, M=Methicnine, N=Asparagine,
Ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	· · · · · · · · · · · · · · · · · · ·
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	sequence	
	Sequence		\=possible nucleotide insertion) RPEKNFDSLESLISAIQGDIEEAKKRLELPEHLKIKEDNFFQVS
1			
6989	2	1118	KSKIMNGH
6989	2	1116	LMPSDRPLSPSTHASAGSECHAPPTTARRAFPIPFGSKSNMATL
1		! !	KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADEL
			ALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKLV
1	!		IITAGARQQEGESRLNLVORNVNIFKFIIPNVVKYSPNCKLLIV
1			SNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
1	}	İ	HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDK
ļ			EOWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLR
ļ	į.		RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE
6000		757	EARLKKSADTLWGIQKELQF
6990	719	258	THASGMASVVLALRTRTAVTSLLSPTPATALAVRYASKKSGGSS
1	}		KNLGGKSSGRRQGIKKMEGHYVHAGNIIATQRHFRWHPGAHVGV
	Į.		GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY
6001	 	<u> </u>	KTFVHVVPAKPEGTFKLVAML
6991	169	453	RRSSDFHNPGFLSRPVSLRENIHHQVICSTKNKRRNPKKIAYLL
]			SSLLMTNLNPNESTENQPVDAYWAFTLDQEFLTYACVEGTGCLF
	ļ <u>.</u>		CGRHVH
6992	941	510	RQAPGCSSLALRQVRQVYCGLVRAPQVQTRPLSSRFVERRGALY
-			RSPMNQENPPPYPGPGPTAPYPPYPPQPMGPGPMGGPYPPPCGY
ļ	1		PYQGYPQYGWQGGPQEPPKTTVYVVEDORRDELGPSTCLTACWT
			ALCCCCLMDMLT.
6993	1	374	QWCVTCPQHNARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG
1			DRVWIKNWNVASLCPLWKGPCTVVLSPPTAVKVEGIPAWIHHSH
		<u> </u>	VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS
6994	346	110C	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALACSR
i	1	·	RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES
ľ			SSQVLWAISSAISVAFFALSGIAAQLLNALGLAGDYLAQGLKLS
i			PGOVQTFLLWGAGALVVYWLLSLLLGLVLALLGRILWGLKLVIF
1		ļ	LAGFVALMRSVPDPSTRALLLLALLILYALLSRLTGSRASGAQL
6995		3346	EAKVRGLERQVEELRWRQRRAAKGARSVEEE
6995	144	1346	GSVNVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL
1	.		LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWACL
1		1	EHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS
	}	1	EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG
			GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL
	!		RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH
	· ·]	HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL
1	1		SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG
	1	ľ	KAIL
6996	543	1040	
0,500	343	1942	ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE
	1		MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLORKSRELLDNEELONLWFLLDKHOTPPMIGEEAMIN
1	1		· · · · · · · · · · · · · · · · · · ·
	1		YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMQFFNY
	1		VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTLPQL
	I		DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD
			LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK
1			EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN
ĺ	[RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD
1		•	PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL
(000	750		NGFWTYENREALVANDSENSADLDDT
6997	370	2104	AMELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPYFLVRF
	[TVIYNEQMASKKRELFSNLQEFAGPSGKLSLLEVGCGTGANFKF
L	1	İ	YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
!	aminc acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	Bedreine	ļ	OVADGSVDVVVCTLVLCSVKNOERILREVCRVLRPGGAFYFMEH
1	Í	i 1	VAAECSTWNYFWOOVLDPAWHLLFDGCNLTRESWKALERASFSK
}			LKLOHIOAPLSWELVRPHIYGYAVK
6998	2	616	FVSRALLRVRSRRHPAEERAAPGRPEDAPIECPGATNCPEPLWC
0330		616	SHLPVPYAPPTMESRGKSASSPKPDTKVPOVTTEAKVPPAADGK
	1		APLTKPSKKEAPAEKQQPPAAPTTAPAKKTSAKADPALLNNHSN
	İ		LKPAPTVPSSPDATPEPKGPGDGAEEDEAASGGPGGRGPWSCEN
	1	İ	
1000		1502	FNPLLVAGGVAVAAIALILGVAFLVRKK
6999	14	1591	GRAGACSRRDTAMSIEIESSDVIRLIMQYLKENSLHRALATLQE
Ì			ETTVSLNTVDSIESFVADINSGHWDTVLQAIQSLKLPDKTLIDL
	ì	l	YEOVVLELIELRELGAARSLLROTDPMIMLKOTOPERYIHLENL
		1	LARSYFOPREAYPDGSSKEKRRAAIAQALAGEVSVVPFSRLMAL
			LGQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFPTQLSRH
	1	[IKFGQKSHVECARFSPDGQYLVTGSVDGFIEVWNFTTGKIRKDL
	1		KYQAQDNFMMMDDAVLCMCFSRDTEMLATGAQDGKI KVWK IQSG
			QCLRRFERAHSKGVTCLSFSKDSSQILSASFDQTIRIHGLKSGK
		ļ	TLKEFRGHSSFVNEATFTQDGHY11SASSDGTVKIWNMKTTECS
Ĭ	1	ĺ	NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNMQ
		į	GQIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV
		1	TGKLERTLTVHEKDVIGIAHHPHQNLIATYSEDGLLKLWKP
7000	2	827	GPGVVFLELMESEGPPESERSEFFSQREEENEEEEAQEPEETGP
į			KNPLLQPALTGDVEGLÇKIFEDPENPHHEQAMQLLLEEDIVGRN
•			LLYAACMAGOSDVIRALAKYGVNLNEKTTRGYTLLHCAAAWGRL
J	j]	ETLKALVELDVDI EALNFREERARDVAARYSQTECVEFLDWADA
ļ	Į.		RLTLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL
			ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH
		<u> </u>	DOKRSODDTSN
7001	2056	844	RRCLIIAFLKGCFIFIYPIFIFETEFLSCCPGWSAVAQSRLIAN
1			FASQVQAIFILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGP
			TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPEANGHRSTNSPTI
1		1	VSFAIVSPTODSRPNMSRPLITRSPASPLNNOGIPTPAQLTKSN APVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ
		1	HYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQL
1			
	1		QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK
	1		SLIEEVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ VLERLOORGFEIVGSCGGGVDSSOFSEYVLRRELRRTPRVPSVI
1			RIKOEPLD
7002	1043	400	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP
1 1002	1043	498	TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS
ł			SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV
1		[
I	,		PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA
7000	618	ļ	RGAEVC
7003	0.18	61	QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP
1	j		GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA
1		[GKOGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP
1		[LLHROVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE
1	1		FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM
			GIKETR\NTRRSIGIEPGAEQLLPNPCPSLEG
7004	121	2285	FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK
1		1	G\PKRTLKTQLG/YYCRVRPLGFPDQECCIEVINNTTVQLHTPE
}		1	GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH
1	1		GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF
1		1	QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ
1	1	1	VDPEFADMITVOEFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL
1			EEVPFDPINPNLHNLNCPVKIKNHNMYVAGCTEVEVKSTEEAFE
1	I	1	VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL

	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	1		H=Histidine, I=Isoleucine, K=Lysine,
1 :	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
1	corresponding	to first	
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence		\=possible nucleotide insertion)
			QEKEQITISQLSLVDLAGSERTNRTRAEGNRLREAGNINQSLMT
	į		LRTCMDVLRENOMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI
	į		VCVNPKAEDYEENLQVMRFAEVTQEVEVARPVDKAICGLTPGRR
ļ		İ	YRNQPRGP\IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRL
}	ļ		IEALEKRHNLROMMIDEFNKOSNAFKALLOEFDNAVLSKENHMO
1		ì	GKLNEKEKMISGOKLEIERLEKKNKTLEYKIEILEKTTTIYEED
1			KRNLQQELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC
l	!	ļ	ERRVAAKOLEMONKLWVKDEKLKOLKAIVTEPKTEKPERPSRER
Ī.			DREKVTORSVSPSPVPVSYL
7005	63	876	RNMALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL
			WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ
1	1		ISSTLADTAVAAOVNGEPYDLERPLETDSDLRFLTFDSPEGKAV
1	}	1	FWHSSTHVLGAAAEOFLGAVLCRGPSTEYGFYHDFFLGKERTIR
	1		GSELPVLERICOELTAAARPFRRLEASRDQLRQLFKDNPFKLHL
			IEEKVTGPTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSS
1			LWRSSG
7006	22	898	NAFGRHSTAVKMAAAAWLQVLPVILLLLGAHPSPLSFFSAGPAT
/000		0,50	VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS
l .			LNITWYLKSADCYNEIYNFKAEEVELYLEKLKEKRGLSGKYQTS
1			SKLFONCSELFKTOTFSGDFMHRLPLLGEKQEAKENGTNLTFIG
j .			DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT
1	1	1	VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR
1			DLLRIOFWIGAVIFLGMLEKAVFYAGFQ
7007	2	1001	AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA
/00/	2	1001	YTQALGLDATPODQAVLHRNRAACHLKLEDYDKAETEASKAIEK
{			DGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKNKVFQEA
	ł		LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKG'PEKKQKAS
ı			QNLVVLAREDAGAEKI FRSNGVQLLQRLLEMGETDLMLAALRTL
			VGICSEHOSRTVATLSILGTRRVVSILGVESQAVSLAACHLLQV
1			MFDALKEGVKKGFRGKEGALIVGEWKQVWGLLDVTVMEGMGLSQ
1			PGQFFGDQTCSCRLFGIRFGDIILL
7008	70	1478	CRSALGHERPPPAHLPAGGRRLQTCPRSCRWLGRPPSGLPPGPR
1,000	1	14/0	SPPPLAGPGQKMVQKKPAELQGFHRSFKGONPFELAFSLDQPDH
1		}	
1		1	- CDCDECLOCGADDOMDACODITIONAKKBCKKKKBCRATNCECC
í			GDSDFGLQCSARPDMPASQPIDIPDAKKRGKKKKRGRATDSFSG
ĺ			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFPEEDRFYLVFEKMRGG
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFPEFEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNNLFESIQEGKYEFPDKDWAHISCAA
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEDRFYLVFEKNRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR
7000			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE
• 7009	1	626	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG
. 7009	1	626	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA
. 7009	1	626	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFPEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAOSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH
. 7009	1 .	626	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFPEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKI I EKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEDRFYLVFEKNRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEAS IYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFES IQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPIMVTPPSAEAH WAVRVEEKAKFDGIFESLEPINGLLSGDKVKPVLMNSKLPLDVLGRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE
7010	79	626	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLNLSMPPKFHDTSSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL GRVWDLSDIDKDGHLVRDEFFVAMHLVYRALE SHTRRAVVPETLLSFLCPLLGGGTAMSGGEQKPERYYVGVDVGT
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE SHTRRAVVPETLLSFLCPLLGGGTAMSGGEQKPERYYVGVDVGT GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKI I EKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS
7010	79	571	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLSGGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT GSVRAALVDQSGVLLAFADQPIKNWEPQFRHHEQSSEDIWAACC VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
7010	79	571	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE SHTRRAVVPETLLSPLCPLLGGTAMSGGEQKPERYYVGVDVGT GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG RIQTLPNQNQSQTQPLLXTPPAVLQPIAPOTTFGVQTQPQPQSL LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP
7010	79	571	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKI I EKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEDRFYLVFEKNRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNNLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLPINGLLSGDKVKPVLMNSKLPLDVL GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC VVTKXVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG RIQTLPNQNQSOTOPLLKTPPAVLQPIAPOTTFGVQTQPQPQSL LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP ARRLDPPSRFSGRNDRGDQVPNRKDDRSREREERRRSRERSPQ
7010	79	571	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE SHTRRAVVPETLLSPLCPLLGGTAMSGGEQKPERYYVGVDVGT GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG RIQTLPNQNQSQTQPLLXTPPAVLQPIAPOTTFGVQTQPQPQSL LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	oogue	\=possible nucleotide insertion)
	Bequence		REVESLEKNMAILDPPDADHLYSAKVMLMASPSMEDLYHKSCAL
			AEDPOELRDGFOHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP
1			DPEKDPSVLIKT\AIRCCKALTG
7012	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGXKAAAA
1 /012	-	2001	AAAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
1			VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
 	ļ		TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
1			NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
1			DRMTSQEAACFPD11SGPQCTQKVFLF1RNRTLQLWLDNPKIQL
1		j 1	TFEATLOOLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
1			PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
1			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKOVNMELAKIKOKCP
1	l		LYEANGOAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
1	j		VSLGQALEVVIQLÇEKHVKDEQIEHWKKIVKTQEELKELLNKMV
	ł		NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
İ			YDELAETOGKLEEKLOELEANPPSDVYLSSRDRQILDWHFANLB
1 .			FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
1			LDIKLNTAVROVRYTASGCEVIAVNTRSTSOTFIYKCDAVLCTL
1			PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
i			FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
1		·	IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
1			RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
1			HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
			AQQSPSM
7013	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
			AAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
			VGERTPRKKEPPRASPPGGLAEPPGSAGPOAGPTVVPGSATPME
			TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
{			NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
			DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLOLWLDNPKIQL
			TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
			PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
}	İ		ATFRKGNYVADLGAMVVTGLGGNPMAVVSKOVNMELAKIKOKCP
1	1		LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGOALEVVIOLOEKHVKDEOIEHWKKIVKTQEELKELLNKMV
1	1	}	NLKEKIKELHOOYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
	1		YDELAETOGKLEEKLOPLEANPPSDVYLSSRDRQILDWHFANLE
1	l		FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
1	1		LDIKLNTAVROVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
1	[PLGVLKOOPPAVOFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
	1		FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
			IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
1			RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
	1		HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
1	1		AQQSPSM
7014	3	3950	DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE
	}		ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEAEEPD
1			CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM
1	1		PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP
	I		HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS
			SVSASRVVKPROSSPOLHNLASYTKKHHTSSVYSISERLEMKPG
	1		POAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP
	İ		DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR
	1		PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRTNAV
			SPKLLSRHRPTCETLEKEGPGHMGRSLDQTSPCPLVLVRIEEME
1	1		RDLDMYSRAQEELNLMLEEKQDESSRAETLEDLKFCESNIESLN
		<u> </u>	

,	Predicted	Predicted end	Amino acid segment containing signal peptide
l .	; beginning ; nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location		Glutamic Acid, F-Phenylalanine, G-Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
l	to firs:	amino acid	P=Proline, O=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
	 		MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIE
l		4	ELLQTERDYIRDLEMCIERIMVPMQQAQVPNIDFEGLFGNMQMV
ŀ	ĺ	[IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDEAIA
ł	1		LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFLIKP
1			VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVNINE
	1	ĺ	YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSHLKH
1		Ì	LTGFAPQIKDEVFEETEKNFRMQERLIKSPIRDLSLYLQHIRES
l		ì	ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNFKER
]		!	TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAEKLK
			DKKTLEELOSARNNYEALNAQLLDELPKFHQYAQGLFTNCVHGY
1			AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSRVLQ
	•	}	QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYMLQSE ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVIKKK
	1		DPMGSQNRWL1DNGVTKGFVYSSFLKPYNPRRSHSDASVGSHSS
1	1	{	TESEHGSSSPRFPRQNSGSTLTFNPN\S\MAVSFTSGSCQKQPQ
ł	1	1	DASPPPKEWDQGTLSASLNPSNSESSPSRCPSDPDSTSQPRSGD
}	ļ	ļ	SADVARDVKOPTATPRSYRNFRHPEIVGYSVPGRNGQSQDLVKG
	1		CARTAOAPEDRSTEPDGSEAEGNQVYFAVYTFKARNPNELSVSA
į.	1	1	NQKLKILEFKDVTGNTEWWLAEVNGKKGYVPSNYIRKTEYT
7015	1842	513	RQAWHE\VAAPSWRGARLVQSVLRVWQVGPHVARERV1PFSSLL
			GFORRCVSCVAGSAFSGPRLASASRSNGQGSALDHFLGFSQPDS
	•	[SVTPCVPAVSMNRDEQDVLLVHHPDMPENSRVLRVVLLGAPNAG
1	1		KSTLSNQLLGRKVFPVSRKVHTTRCQALGVITEKETQVILLDTP
	}		GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTRN
1	:	[QLSPQLLRCLTKYSO1PSVLVMNKVDCLKQKSVLLELTAALTEG VVNGKKLKMRQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIGWPH
[Į.	FKE1FMLSALSQEDVKTLKQYLLTQAQPGPWEYHSAVLTSQTPE
l	:	}	EICANIIREKLLEHLPQEVPYNVQQKTAVWEEGPGGELVIQQKL
	:	1	LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRLSV
	!		KLTK
7016	167	2513	ILNAPKPPPPRDSVEAVAAKRDTGGGSWGTGMDVSGQETDWRST
		}	AFROKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYLS
		ĺ	LVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAAGIGM
	1	1	PPRGPGQSLGGMGSLGAMGQPMSLSGQPPPGTSGMAPHSMAVVS
		1	TATPOTOLOLOQVAAAAAATARSSSSSRRAYSSSSSSNSKQ
1	t	1	FQAQQSAMQQ\QFQA\VVQQQQQL\QQQQQCQHLIKLHHQNQQ
	1		QIQQQQQLQRIAQLQLQQQQQQQQQQQQQQCOALQAQPPIQQP PMQQPQPPPSQALPQOLQQMHHTQHHQPPPOFOOPPVAQNQPSQ
ĺ	•	Í	LPPOSOTOPLVSOAOALPGOMLYTOPPLKFVRAPMVVQQPPVQP
}		}	QVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP
}		j .	OSMPPPPOPSPOPGOPSSOPNSNVSSGPAPSPSSFLPSPSPQPF
			\QSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQY
1		!	LDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILTDP
}		1	SKRCPLKTLQKCEIALEKLKNDMAVPTPPPPPPVPPTKQQYLCQP
]	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR
	•		RLEDDERQSIPSVLQGEVARLDPXFLVNLDPSHCSNNGTVHLIC
	•	!	KLDDKDLPSVPPLELSVPADYPAOSPLWIDROWQYDANPFLQSV
	}		HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA
7017	1	1785	INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL
ĺ	:	{	FAFLAHTQREAYAPRIFFEASRPPWFTPRSQCDCSEYLRFLLDR
1	•	ł	LHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETPRTS
			DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEAFTDLSLAFWPS
	•]	YSLEYMSCPDCSOSPSIQDGGLMQASVPGPSEEPVVYNPTTAAF
}	:		ICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPQKPG
1	1		GETTPSVTDLLNYFLAPEILTGDNQYYCENCASLQNAEKTMQIT EEPEYLILTLLRFSYDQKYHVRRKILDNVSLPLVLELPVKRITS
L		<u> </u>	CELETIPIPIPIKESINAVIUAKKKIPDUASPAPAPEDAAKKIIS

·			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	
l	1	1	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
\	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEASCTKLVPYLLS
{	1		SVVVHSGISSESGHYYSYARNITSTDSSYOMYHOSEALALASSO
			SHLLGRDSPSAVFEODLENKEMSKEWFLFNDSRVTFTSFOSVOK
1	1	1	ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGLWINGDPPLQKE
l	1	Į.	LMDAITKDNKLYLQEQELNARARALQAASASCSFRPNGFDDNDP
j	1	į.	1
			PGSCGPTGGGGGGFNTVGRLVF
7018	484	1066	SLVFRGNTWSGEAGHHCSALFNLAAYHOLFVGTER1RAPE11FQ
1	ì)	PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQNVFLTGGNTMYP
Į.	1		GMKARMEKELLEMRPFRSSFQVQLASNPVLDAWYGARDWALNHL
į			DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIRLPKQASRSSDA
}	1	1	OASSKGSAAGGGGAGEOA
7019	1048	335	APGGFLVTMVFPAPSPPWMLGCCSHEVTAGPPTLCKDMSALVAA
1 .33	1010)	RMRHIPLAPGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNGRS
ļ	{	į.	1
			SSGALRGVCSCVEAGKACDPAAROFNTLIPWCLPHTGNRHNHWA
}	1	}	GLYGRLEWDGFFSTTVTNPEPMGKQGRVLHPEQHRVVSVRECAR
4	I		SQGFPDTYRLFGNILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK
}	1]	ARESASAKIKEEEAAKD
7020	1	2154	FADSKRKSVLLDKIKNLQVALTSKQQSLETAMSFVARNTFKRVR
Ì	1	1	NGFLMRKVAVFFSNTPTRASPOLREAVLKLSDAGITPLFLTRQE
1			DROLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDIC
ł			NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFQF
1	1		NEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQHAPSESVDNAS
1	1	<u> </u>	1
1	1		MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGSAIEYTI
ì	1		ENVFESAPNPROLKIVVLMLTGEVPEOOLEEAORVILQAKCKGY
[1	l	FFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLMR
1	1	ļ	FGRLLPSFVSSENAFYLSPDIRKQCDWFQGDQPTKNLVKFGHKQ
1	1		VNVPNNVTSSPTSNPVTTTKPVTTTKPVTTTTKPVTTTTKPVTI
1	1	{	INQPSVKPAAAKPAPAKPVAAKPVATKTATVRPPVAVKPATAAK
1	Ĭ	}	PVAAKPAAVRPPAAAAAKPVATKPEVPRPQAAKPAATKPATTKP
l	1	-	MVKMSREVQVFEITENSAKLHWERPEPFGPYFYDLTVTSAHDQS
[1		LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS
1	ł		TKKSOPPPPOPARSASSSTINLMVSTEFLALTETDICKLPKDEG
1	1	1	TCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA
]			_
<u></u>	ļ	L	PVLAKPGVISVMGT
7021	2	338	VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG
i	1		ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS
	I		CLGVTDDGMAVATGSWDSFLRIWN
7022	2	856	VYIGSFWSHPLLIPDNRKLFEAEEQDLFRDIQSLPRNAALRKLN
ł		-	DLIKRARLAKVHAYIISSLKKEMPSVFGKDNKKKELVNNLAEIY
1			GRIEREHOISPGDFPNLKRMODOLOAODFSKFQPLKSKLLEVVD
	1	1	DMLAHDIAOLMVLVROEESORPIOMVKGGAFEGTLHGPFGHGYG
			EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM
1		1	
		1	VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH
L	1	L	ELPNELPAHLLPPSKRKVAE
7023	2	748	AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF
	Į	Į.	WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF
1		1	TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG
1		}	VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST
	}	1	EGMS I KMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA
]	1		ILGOAYAFARHPOKPAPHAVHPTGTKAL
7004	1202	 	
7024	1207	190	RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV
		1	SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS
1		1	QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT
]		1	RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD
1		4	FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV
1	1	1	VROLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL
		1	

CEO	Predicted	Dredicted and	Three acid compart containing cignal nontice
SEQ	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (L=Alanine, C=Cysteine, D=Aspartic Acid, E=
-	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	Į.	Hawistidine, Ialsoleucine, Kalvsine,
}	1	corresponding to first	1
1	corresponding	amino acid	LeLeucine, M=Methionine, N=Asparagine,
	tc first	1	Paproline, O=Glutamine, R=Arginine,
	amino acid	residue of	SaSerine, TaThreonine, Valline,
	residue of	amino acid	Walryptophan, YaTyrosine, XaUnknown, *=Stop
}	amino acid	sequence	Cocon, /=possible nucleotide deletion,
	sequence	<u> </u>	\~possible nucleotide insertion)
1	}	}	TGSTKQVAQASHSYRVYYNAGPKDEDQDYIVDHSIAIYLLNPDG
2005			LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS
7025	232	832	ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNQEECF
	1		KOVIRTCEKRPTFNQHTVFNLHQRLNTGDKLNEFKELGKAFISG
{	1	[SDHTQHQLIHTSEKFCGDKECGNTFLPDSEVIQYQTVHTVKKTY
1		}	ECKECGKSFSLRSSLTGHKRIHTGEKPFKCKDCGKAFRFHSQLS
			VHKRIHTGEKSYECKECGKAFSCG
7026	328	1146	NPNPSIGDIKDIKKAAKSMLDPAHKSHFHPVTPSLVFLCF1FDG
j]	1	LHQALLSVGVSKRSNTVVGNENEERGTPYASRFKDMPNFIALEK
}	1	1	SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS
]	1	HGESADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK
1	!	1	LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE
	1		EKKVNG*KGIGEIF*VWGCTLPPHYWGAVTTNVPKLSNSGKLLG
		<u> </u>	QDEQPHIFG
7027	43	954	GRRLQQQQRPEDAEDGAEGGGKRGEAGWEGGYPEIVKENKLFEH
1			YYOELKIVPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL
1			KNKYFKELEDLEMDGQKVEVPQPLSWYPEELAWHTNLSRKILRK
1	į		SPELEKFHQFLVSETESGNISRQEAVSMIPPLLLNVRPHHKILD
1	į.		MCAAPGSKTTQLIEMLHADMNVPFPEGFVIANDVDNKRCYLLVH
1	ł		QAKRLSSPCIMVVNHDASSIPRLQIDVDGRKEILFYDRILCDVP
			CSGDGTMRKNIDVWKKWTTLNSLQLHGLQLRIATRGAEQL
7028	189	608	SRFPPEPEPGTMVEKGSDSSSEKGGVPGTPSTQSLGSKNFIRNS
1			KKMCSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQR
1	1		EILLOGRLYLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA
		<u> </u>	KL1 PNAIQ
7029	1343	40	VLESNTEAKQATGTSSKLRHGTGQEKGREGPRCPSGLAQLRLWG
1			/PCPHAGRETGPRASAPIPGS*GHGWHW*RKDGRGERSEGPSAL
1			SPHSPSLLNMQQAPTHVGPGMGSQRPRSSVVPEQVGVGSQLSRE
1			RWRA*RSLPGAAASERTEMTKERSP/RPCCGYDSSNWFTQPGKK
1	ł	1	TRKRNSRRNTMVSRGGGCLLYPLQSIMPE*QLR*GAHASPPTQG
			R*GKGGPRSPLTKASGTTHIPTPFFGSIP/RPTRDSGFGTDNS\
}		1	AAPGOKRGHREA*QGPEPV/WGRVTTHLOGPAG*TKPLGS\RNW VPGPAEGEQGEGAGLEGRP*PLKGCRSTLTFSPQLSIPMVGKKP
1			PEGTTASFFP\RSCHSE*RKPPPSCPHAPALSLPHPLPLPPL
}	1		PLFLPGAGT*HSARSGRPGOSETGSLCHNCHHCPPHCPKCSPGG
}		1	m
7030	2	521	FVCFSAPGSGQGGKRRVNMELSAVGERVFAAEALLKRRIRKGRM
,030	-	321	EYLVKWKGWSOKYSTWEPEENILDARLLAAFEEREREMELYGPK
1			KRGPKPKTFLLKAQAKAKAKTYEFRSDSARGIRIPYPGRSPQDL
1		1	ASTERAREGLEN\RVCPRORAAPAFAAP\PRRGPSGPGPRPG*G
i	1,		PGL-HFPGPGGPSKHGFVPASEOHOHOOHLPRRGPSGPGPRPG
7031	960	59	HCSVPGAEWPRKPFAQICPQLTSRPHLSSPRSLSPGCGHSPGPG
1 ,031	1 200	1	/CKPS/RHCDELHEGPSRTAALPCGKPOPKHGVEECG/PCPCLA
1		ł	PRRLTEPPALTVSPVGRAAPSGAL*PSGRACSACSHRLAPEAAL
1	}		SAAAPRPSLGSGQNASGLPAASLPPQDSSQPHKTVPSPARSVPP
1	1	1	LGACARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGPTPST
	1	1	SGSTASHSRRGC*SPR*TPAPPRRDHGRSAAFEVLTAAASAQPC
1	1	1	ASOGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCRHPSL
7032	1202	2102	
1032	1393	2104	RRPGRTEPVEPPPVPPPPRASNSKSRCR*RNLHLAPL*QSPLRK
İ			SROIGTSSLPFGRSAGERPRPAATFCLSRGGSSPVFL*PSSSSL
1	1	1	EPWMKRQFGRLHSLFWKSWQKMNSFLLTPKLDTSLMSGWRYRQR
1			LPRLHTFLKKSLQMASELAPPLPTPAPLASSLPPPPGPPPLLPV
1	1	1	PLA*LSRSGILVPPNSGFSLSC\PLGDH*GSSGEVRGSCGSPPP
1			
7033	689	815	HHCWVLPPPP*LLLPPR RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA

			,
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
(location .	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acić	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
		 	LMMPSSCPWRTGALGPSPAGSRALGRCTSSVGPGSRWLTRTSSP
1	}		GCATRTWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS
1	}		AAAPSAPTTPAAAGPNTL*SRRTAEWCWPPSCSCCWGWC*SWSA
İ	1		WDWRRPPLQVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS
Į			SSSTCPTSRSDRGAAWTP\SPMGAPLLPCSVPLISREEALODPR
1			NPSP*GVCSGSSGHAGLALGKPPVACSVP
7024		7.040	<u> </u>
7034	92	1942	EDTSSMPFRLLIPLGLLCALLPOHHGAPGPDGSAPDPAHYRERV
			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
	1		TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
1	†	}	RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
1	1		FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
1	1	Į.	TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
1	1	1	IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
	ļ		YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
Ì		1	TVWKQFGGLPEFYNIFQGYTVEKREGYPLRPELIESAMYLYRAT
1	1	1	GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
1			FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
İ			FNTEAHPIDPAALHCCORLKEEOWEVEDLMREFYSLKRSRSKFO
		1	KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
		İ	QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
ì			K
7035	92	1942	EDTSSMPFRLLIPLGLLCALLPOHHGAPGPDGSAPDPAHYRERV
			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
İ		<u> </u>	TLL\TLFYFQILGNVSEFORVVEVLQDSVDFDIDVNASVFETNI
1	1	•	RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
			FOTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
1	Ì	ì	TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
			IGAGVDSYFEYLVKGAILLODKKLMAMFLEYNKAIRNYTRFDDW
-	1	1	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
1		i i	TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
į	į.		GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
ŀ			
Í	ĺ		FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
1]	Ì	FNTEAHPIDPAALHCCORLKEEQWEVEDLMREPYSLKRSRSKFQ
1	1	1	KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
1		1	QPFTSKLALLGQVFLDSS*PLDNFF1F1FLRLNYNKLLLA11KK
L			K
7036	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
1			RNW*ERKAGCSQPC/PACQHHGRPPGVSPLPRDPHPTTLRPLPP
L	<u></u>		PPPPPPPPPRRPPRNRRPG
7037	442	761	CLAPLFSCFQ11NLHLAPSGRLRWAWLRGPGRN*LPGEGPS1PT
]	RNW*ERKAGCSQPC/PAQOHHGRPPGVSPLPRDPHPTTLRPLPP
ļ	1	!	PPPPPPPPPPRRPPRNRRPG
7038	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
[[QYNKLLEKSDLHSVLAOKLQAEKHDVPNRHEISPGHDGTWNDNQ
1	1	1	LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
1		1	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
1	1	1	LOITFTALEGKLRKTTEENOELVTRWMAEKAQEANRLNARE*KR
1	1	1	LQEAASPAAERACRSSKGTSTSRTG
7039	155	891	GAGAASDMSSGLRAADFPRWKRHISEOLRRRDRLQRQAFEEIIL
1	1	""	QYNKLLEKSDLHSVLAOKLQAEKHDVPNRHEISPGHDGTWNDNQ
]	1	1	LOEMAOLRIKHOEELTELHKKRGELAO\RVIDLNNQMQRKDREM
1	1	j	
	1	1	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
1	1	1	LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
L			LQEAASPAAERACRSSKGTSTSRTG
7040	34	789	KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS GYESVMRDSEATGSASSAODSTSENSSSVGGRCRSLKTPKKRSN

SEC	Predicted	Predicted end	Amino acid segment containing signal peotide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
•	corresponding	to first	L=beucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codor., /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
	Sequence	ļ	PGSQRRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRSSPRGLG
1			EPFEIKVYEIDDVERLORRRGGASKEAMCFNAKLKILEHROORI
			AEVRAKYEWLMKELEATKOYLMLDPNKWLSEFDLEOVWELDSLE
			YLEALECVTERLESRVNFCKAHLMMITCFDIT
7041	2	567	SGRVAMGRRRAPAGGSLGRALMRHQTQRSRSHRHTDSWLHTSEL
/031	<u> </u>	367	NDGYDWGRLNLOSVTEOSSLDDFLATAELAGTEFVAEKLNIKFV
i	1]	PAEARTGLLSFEESQRIKKLHEENKQFLC1PRRPNWNQNTTPEE
1	l .	;	
1		•	LKQAEKDNFLEWRROL\VRLEEEQKLILTPFERNLDFWRCLWRV
7042	7	946	IERSDIVVQIVDA
1032	1 '	345	PIHMAAAALRADI\ISPLFPHIQGYLLLSASHG\ATSLATKGAL
	1		PLETVTMYTVIPKSKYVLVKPDTQYPYSENLDEFKRLAENSASN
7043	2	. 22.20	DDLLMAEVAISDYGDKLTLELREKY
1043	1	2170	ARGMAARDSDSEEDLVSYGTGLEPLEEGERPKKPIPLODOTVRD
	1	(EKGRYKRFHGAFSGGFSAGYFNTVGSKEGWTPSTFVSSRONRAD KSVLGPEDFMDEEDLSEFGIAPKAIVTTDDFASKTKDRIREKAR
1			KSVLGPEDFMDEEDLSEFGIAPKAIVTTUDFASKTKDRIKEKAR QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMGWKEGCGVGP
ľ			RVKRRPRROKPDPGVKIYGCALPPGSSEGSEGEDDDYLPDNVTF
			APKDVTPVDFTPKDNVHGLAYKGLDPHOALFGTSGEHFNLFSGG
Ì	· I]	
1	Í	1	SERAGDLGEIGLNKGRKLGISGQAFGVGALEEEDDDIYATETLS
			KYDTVLKDEEPGDGLYGWTAPRQYKNQKESEKDLRYVGKILDGF SLASKFLSSKKIYPPPELPRDYRPVHYFRPMVAATSENSHLLOV
ł]		LSESAGKATPDPGTHSKHOLNASKRAELLGETPIQGSATSVLEF
Į	ļ		LSOKDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA
i	İ	1	AGHCSWNMALGGGTATLKASNFKPFAKDPEKOKRYDEFLVHMKQ
1			GOKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLSSRF
i	1		THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLTRDTFEW
			HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTOASSE
1	1		KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK
}	j		QQSSPLVNKEEEHAPELSAN
7044	276	734	EVYLTDEFAKGRKVADLYELVOYAGNIIPRLYLLITVGVVYVKS
''''	1	123	FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG
l	1	İ	EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR
	}		EREROELRILVGTNLVRLSOV
7045	3	513	LGFKMEALSRAGOEMSLAALKOHDPYITSIADLTGOVALYTFCP
1	1		KANQWEKTDIEGTLPVYRRSASPYHGFTIVNRLNMHNLVEPVNK
	1		DLEFOLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
	1		ETRRSOOA/RSGOTESOPGOWLORPOAHRHPGDAEOSOG
7046	3	513	LGFKMEALSRAGOEMSLAALKOHDPYITSIADLTGOVALYTFCP
1	1		KANOWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
	1	1	DLEFOLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
ļ		1	ETRRSOOA/RSGOTESOPGOWLORPOAHRHPGDAEOSOG
7047	103	486	OMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN
	1	1	IMLIDVREIWEILEYOKIPESINVPLDEVGEALOMNPRDFKEKY
	1		NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER
7048	92	627	FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY
	1	\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \	WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQ1ETRN
	ļ		RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA
		1	l
	1		IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI
7049	303	n20	EKKW PROCEDURE CODAMA CUA CROCCUCK I DADROVEDDI
1013	393	938	KRTGSASYGGPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL
	İ		VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
1	!	Ì	NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT
1	ļ		EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKL1AWX
7050			ASSLWG
7050	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL

SEQ	Fredicted	Predicted end	Amino acid segment containing signal peptide
ID	becinning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
No.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparacine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	
(1		S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u> </u>	\=possible nucleotide insertion)
ļ	}		VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
i	}		NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT
}	}	ł	EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG
7051	119	816	KKMNLAEICDNAKKGREYALLGNYDSSMVYYOGVMQOIQRHCQS
l	1		VRDPAIKGKWQQVRQELLEEYEQVKSIVGTLESFKIDKPPDFPV
}	1		SCODEPFRDPAVWPPPVPAEHRAPPQIRR/ROSESKTSEERNGR
1	į		SRSPGTCRPST\PISKSEKPSTSRDKDYRARGRDDKGRKNMQDG
I			ASDGEMFKFDGAGYDKDLVEALERDIVSRNPSIHWDDIADLEEA
1			KKLLREAGVL?MWM
7052	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
	1		TYRNSMYHNKHVFKDKVVDDVGSGTGILSMFAAROGPRR
7053	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
, 553	1 30'	(13	TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAAROGPRR
7054	 	1026	GTSQRSRETDARRRSAGAEPTARLPWPAALEEWPSCPCEPLGPG
, , , ,	1 -	1036	RRCRWDAMEYDEKLARFROAHLNPFNKOSGPROHEOGPGEEVPD
1			
İ		ļ	VTPEEALPELPPGEPEFRCPERVMDLGLSEDHFSRPVGLFLASD
1		1	VQQLRQAIEECKQVILELPEQSEKQKDAVVRLIHLRLKLQELKD
((PNEDEPNIRVLLEHRFYKEKSKSVKQTCDKCNTIIWGLIQTWYT
l			CTGCYYRCESKCLNLISKPCVSSKVSHQAEYELNICPETGLDSQ
}	j	į	DYRCAECRAPI/CS/DGVVPSEARQCDYTGQYYCSHCHWNDLAV
L			IPARVVHNWDFEPRKVSRCSMRYLALMVSRPVLRLREIN
7055	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
}	1	•	EYHYLHOMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
Į	l		SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
1	ł		FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
			M
7056	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
			EYHYLHQMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
}	İ		SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
ļ	į.	Į.	FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
ŀ			М
7057	1368	431	GIYLHVNEKIFRPTCIGDRQENDKENLNLENHRDQELLHASCQA
			SGEVPSOASLRGFFTEDEPGCFGEGENLPEALQNIODEGTGEQL
1.	1	!	SPQERISEKQLGQHLPNPHSGEMSTMWLEEKRETSQKGQPRAPM
1		· ·	AQKLPTCRECGKTFYRNSQLIFHORTHTGETYFOCTICKKAFLR
1		1	SSDFVKHORTHTGEKPCKCDYCGKGFSDFSGLRHHEKIHTGEKP
]	1	r	YKCPICEKSFIQRSNFNRHQRVHTGEKPYKCSHCGKSFSWSSSL
İ	1		DKHORSHLGKKPPQ+PVTKLSFPISISOPSHKNTOLHQEELCLR
	1		GYPC
7058	1	469	FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRALCCKGPPPAR
1	_	1	PEYDLVCIGLTGSGKTSLLSKLCSESPDNVVSTTGFSIKAVPFO
j	}		NAILNVKELGGADNIRKYWSRYYQGSQGVIFVLDSASSEDDLEA
			ARN*SCTOLLOHPOLCTLPFLILA
7059	 	1178	WPAFPRQPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA
,,,,,	1 4	11/0	
j	1		APWARPSAWLECVCVVTFDLELGQALELVYPNDFRLTDKEKSSI
Į.	Į.		CYLSFPDSHSGCLGDTOFSFRMRQCGGQRSPWHADDRHYNSRAP
			VALOREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL
1			FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAPAPGQTLNLPVM
1	[GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF
			RCFRPVLTHMQTLWELMLLGEPLLVLAFSPDVSSEMVLALTSCL
1	}	1	QPLRFCCDFRPYFTIHDSEFKEFTTRTQAPPNVVLGVTNPFFIK
	1		TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP
7060	90	1670	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ
1		1	YRFEHLVTOMKWRLOEGRGEAVYOIGVEDNGLLVGLAEEEMRAS
		1	

SEO I	Predicted	Predicted end	Amino scid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, FaPhenylalanine, GaGlycine,
Į.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	b=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, C=Glutamine, R=Arcinine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Coaon, /=possible nucleotide deletion,
i J	sequence	ooguonee	\=possible nucleotide insertion)
	- og-onec		LKTLHRMAEKVGADITVLREREVDYDSDMPRKITEVLVRKVPDN
			QQFLDLRVAVLGNVDSGKSTLLGVLTQGELDNGRGRARLNLFRH
			LHEIQSGRTSSISFEILGFNSKGEVHGINGTQWGQTLRMGW***
			RT+DGGRVWRLFEIV+MNALRGL+TSSAPLRKSMGNOLN+IKNG
1			VKIKROCHPENGLEPENSEGVGRAGRRH. GPWALGOVVNYSDSR
1	'		
			TAEEI CESSSKMITFI DLAGHHKYLHTTI FGLTSYCPDCALLLV
			SANTGIAGTTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR
l			QLERVLKQPGCHKVPMLVTSEDDAVTAAOQFAQSPNVTPIFTLS
			SVSGESLDLLKVFLNILPPLTNSKEQEELMQQLTEFQVDEIYTV
	764	7-2-	PEVGTVVGGTLSR*IDLLATLPTQPSPIYSKTSWPKGGDPGI
7061	364	710	ARMPSPLGPPCLPVMDPETTLEEPETARLRFRGFCYQEVAGPRE
			ALARLRELCCOWLOPEAHSKEQMLEMLVLEQFLGTLPPEIQAWV
			RGQRPGSPEEAAALVEGLQHDP+ARMPSFLGPPCLPVMDPETTL
			EEPETARLRFRGFCYQEVAGPREALARLRELCCQWLQPEAHSKE
			OMLEMLVLEOFLGTLPPEIQAWVRGQRPGSPEEAAALVEGLCHD
			PGQLLG
7062	71	744	AKAGTNLERLHWLSYFFCIPKHKLKSSQKDKVRQFMACTQAGER
)			TAIYCLTQNEWRLDEATDSFFQNPDSLHRESMRNAVDKKKLERL
			YGRYKDPQDENKIGVDGIQQFCDDLSLDFASISVLVIAWKFRAA
			TOCEFSRKEFLDGMTELGCDSMEKLKALLPRLEQELKDTAKFKD
			FYQFTFTFAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL
			менн
7063	2	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR
1			LTEYIHCLQPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF
ł l			FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA
			EYNMSCDDTGKLILKPRPHVQ*QSSLIVMGLKIAFLRISDTAKS
	200		HKGFLLRLDM ·
7064	300	884	RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS
			SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC
			SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR
			CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP
			PLLTPLGAGRAGGSRANS
7065	1	555	ATTTHSARRSGRGAAAEAAASAAGGRQKGFDRKAWEGRRTTPGG
			RSQSEPKAPPPQKRSEAAFASMAHSPVAVCVPGMQNNIADPEEL
			FTKLERIGKGSFGEVFKGIDNRTQQVVA1KIIDLEEAEDEIEDI
	1-		QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL
7055	355		RAGPFDEFQ
7066	356	676	PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT
			YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND
70.53			VGVEVGGSGGCLEERTPP
7067	152	973	KENITMATEIGSPPRFFHMPRFQHQAPROLFYKRPDFAQQQAMQ
		İ	OLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ
		Į.	PDAGYYNDI, VPPI GML, NNPMNAVTTKFVRTSTNKVKCPVFVVRW
			TPEGRRLVTGASSGEFTLWNGLTFNFETJLQAHDSPVRAMTWSH
			NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP
			FSVVPIVMVKLFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT
			HSPFCWAPF
7068	222	816	DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD
			DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
			VHCSDLGLTSVPTNIPFDTRMLDLQNNK1KEIKENDFKGLTSLY
			GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL
ı İ		l	AELRIHENKVKKIQKDTPKKK
) }		1	
7069	1147	1765	FRDHRRYFYVNEQSGESQWEFPDGEEEEEESQAQENRDETLAKQ
7069	1147	1765	l —

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	seducince	\=possible nucleotide insertion)
	Rednettice		
		1	EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDEEDNSSSSEED
		<u> </u>	RVSTAQKRIEEWKQQQLVSGMAERNANFEA
7070	3	547	DGTMEDSEAVQRATALIEQRLAQEEENEKLRGDARQKLPMDLLV
		1 .	LEDEXHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLI
			ELRKKRKCKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGK
		ļ	MKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG
			ATVDFQ
7071	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
		1	VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
		1	FODPRTOIPFEVPOYPOTGYYPPPPTVPAGVAPCVPRFVRSNNV
		1	PESSI.PPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
			PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
			SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ
	L	<u> </u>	IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7072	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
	}	}	VSNVAATSAGPSNVGTELNSVPOKSSPFLTRVPAYPPHSENIQY
			FODPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
		1	PESSLPPASMPYADHYSTFSPRDRMNSSPYCPPPPQPYGPVPPV
	}	}	PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
		1	SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ
i	İ		IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7073	50	504	LAHGSFGVSDFPAPAAAPAHTLTSFSGSLSPOFRKPLGRAPAMP
		}	LVRYRKVVILGYRCVGKTSLAHOFVEGEFSEGYDPTVENTYSKI
	ĺ	1	VTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSVTSL
		1	HSFQVIESLYQKLHEGHGK
7074	263	1003	VCPVLCSTRQEPGHSSLVTYFGKPTRRKEFLLGHCIAAGKMNIS
	Į.		VDLETNYAELVLDVGRVTLGENSRKKMKDCKLRKKQNERVSRAM
	Į.		CALLNSGGGVIKAEIENEDYSYTKDGIGLDLENSFSNILLFVPE
	ĺ	l	YLDFMQNGNYFLIFVKSWSLNTSGLRITTLSSNLYKRDITSAKV
	(ļ	MNATAALEFLKDMKKTRGRLYLRPELLAKRPRVDIQEENNMKAL
			AGVFFDRTELDRKEKLTFTESTHVEI
7075	598	1005	NYINFFFRKEYPPHVQKVEINPVRLSRLQGVERIMKKTEESESQ
	1	{	VEPEIKRKVQQKRHCSTYQFTPPLSPASKKCLTHLEDLQRNCRQ
	{	1	AITLNESTGPLLRTSIHQNSGGQKSQNTGLTTKKFYGNNVEKVP
		<u></u>	IDII
7076	279	1049	LOSESSNAAEGNEQRHEDEQRSKRGGWSKGRKRKKPLRDSNAPK
			SPLTGYVRFMNERREQLRAKRPEVPFPEITRMLGNEWSKLPPEE
	f	1	KORYLDEADRDKERYMKELEQYQKTEAYKVFSRKTQDRQKGKSH
	1	}	RODAARQATHDHEKETEVKERSVFDIPIFTEEFLNHSKAREAEL
	1	1	RQLRKSNMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV
	L		LQQHLETLRQVLTSSFASMPLPEXGETPTVDTIDSYM
7077	3	1119	SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR
	1	1	ELKWLDMFSNWDKWLSRRFOKVKLRCRKGIPSSLRAKAWQYLSN
	1	1	SKELLEONPRKFEELERAPGDPKWLDVIEKDLHROFPFHEMFAA
	ì		RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ
		1	AFWCLVQICDKYLPGYYSAGLEAIQLDGEIFFALLRRASPLAHR
	1	1	HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI
	1	1	IFRVALVLLRHTLGSVEKLRSCOGMYETMEQLRNLPQQCMQEDF
	1		LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS
	1		RAIHEERRRQQPPLGPSSS
7078	483	767	FOGORMAGEOKPSSNLLEOFILLAKGTSGSALTALISQVLEAPG
	103	1	VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE
	1	Į.	1 Conntration and analynamic
	į.	i	I CT.DET.V
7079	2	376	SUPELY SVVEFKRPKEPSGSDGESDGP1DVGQEGQLSQMARPLSTPSSSQ

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SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	
NO:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
		to first	1
	corresponding	I .	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	to first	amino ació	
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acić	sequence	Codon, /=possible nucleotide deletion,
	redneuce	<u> </u>	\=possible nucleotide insertion)
			AEVLQMTVDHLKMLHATGGTGTHALLFQASFIQQ1F
7080	200	595	VQLPLEAPCLSLLSCRDHSGGNRDLSRRHRDCRVYGSPQDG1PY
i	}		LTHPLCHQDVVSVGRLQIRALATPGHTQGHLVYLLDGEPYKGPS
			CLFSGDLLFLSGCGEFPRKREELGEEGETEVRAATVPWRALKP .
7081	213	506	AVTEEEMILNSLSLCYHNKLILAPMVRVGTLPMRLLALDYGADI
		1	VYCEELIDLKMIQCKRVVNEVLSTVDFVAFDDRVVFRTCEREQN
	_		RVVFQMGTS
7082	3	1137	APSRNTMLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSL
			CCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSISDIGTGCL
			SSLENLRLPTLREESSPRELEDSSGDQGRCGPTHQGSEDPSMLS
	ļ		QAQSATEVEERHVSPSCSTSRERPFQAGELILAETGEGETKFKK
			LFRLNNFGLLNSNWGAVPFGKIVGKFPGQ1LRSSFGKQYMLRRP
			ALEDYVVLMKRGTAITFPKDINMILSMMDINPGDTVLEAGSGSG
			GMSLFLSKAVGSQGRVISFEVRKDHHDLAKKNYKHWRDSWKLSH
	1		VEEWPDNVDF1HKDISGATED1KSLTFDAVALDMLNPHVTLPVF
			YPHLKHGGVCPVYVVNITQVIELLD
7083	115	541	RSNAVQLTRMEYAMKSLSLLYPKSLSRHVSVRTSVVTQQLLSEP
	}		SPKAPRARPCRVSTADRSVRKGIMAYSLEDLLLKVRDTLMLADK
			PFFLVLEEDGTTVETEEYFQALAGDTVFMVLQKGQKWQPPSEQG
			TRHPLSLSHK
7084	3	522	NSVSVSSQSRFLASVPGTGVQRSAAADMAASTAAGKQRIPKVAK
	[VKNKAPAEVQITAEQLLREAKERELELLFPPPQQKITDEEELND
•			YKLRKRKTFEDNIRKNRTVISNWIKYAQWEESLKEIQRARSIYE
	İ	Į	RALDVDYRNITLWLKYAEMEMKNRQVNHARNIWDRAITTL
7085	243	1499	RQLARLRRRGWRSPFGGAPMAHITINQYLQQVYEAIDSRDGASC
			AELVSFKHPHVANPRLOMASPEEKCOOVLEPPYDEMFAAHLRCT
			YAVGNHDFIEAYKCQTVIVQSFLRAFQAHKEENWALPVMYAVAL
			DLRVFANNADQQLVKKGKSKVGDMLEKAAELLMSCFRVCASDTR
	ł		AGIEDSKKWGMLFLVNQLFKIYFKINKLHLCKPLIRAIDSSNLK
			DDYSTAQRVTYKYYVGRKAMFDSDFKQAEEYLSFAFEHCHRSSQ
	1		KNKRMILIYLLPVKMLLGHMPTVELLKKYHLMQFAEVTRAVSEG
			NLLLHEALAKHEAFFIRCGIFLILEKLK]ITYRNLFKKVYLLL
	1		KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGYI
}	}		SHQHQKLVVSKQNPFPPLSTGC
7086	256	525	ILAARMGKONSKLRPEVMODLLESTDFTEHEIQEWYKGFLRDCP
			SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGDGTIDFR
	1		EF
7087	166	723	LSGSSAGKVAAPCVPPSNHELVPITTENAFKNVVDKGEGASRGG
	1		NTRKSLEDNGSTRVTPSVQPHLQPIRNMSVSRTMEDSCELDLVY
ł	Į.	{	VTERIIAVSFPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLS
1			ERRPDITKLHAKVLEFGWPDLHTPALEKICSICKAMDTWLNAHP
			HRCRVLHNKG
7088	104	759	GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT
1	1		MPKAFATAGWLVSLVLLVFLGFMSFMTTTFVIEAMAAANAQLHW
			KRMENLKEEEDDDSSTASDSDVLIRDNYERAEKRPILSVQRRGS
	1		PNPFEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDLAIYA
İ	1		AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD
7089	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
1	""	1	HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
}	1		SPIHTSVOFOASYLPKPGAOLYOFRYVNROGOVCGOSPPFOFRE
			PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
	1	ļ	QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS
Ì		Į	HGEITEERDILSROOGDHVARILELEDDIOTISEKVLTKEVELD
1]		RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELQVAQQENHHL
	4_	ŀ	NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptice
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanino, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:		1	
t	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T≈Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
í	sequence	1 -	\=possible nucleotide insertion)
			LKEOLRGAOELAASSOOKATLLGEELASAAAARDRTIAELHRSR
Ĭ		ł.	LEVAEVNGKLAELGLHLKEEKCOWSKERAGLLOSVEAEKDKILK
			LSAEILRLEKAVOEERTONOVFKTELAREKDSSLVQLSESKREß
İ			TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
Į.		l	EDATTEDEEAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETO
			7
			ASLLLGLE
7090	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
- 1			HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
(}	SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE
			PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
		1	QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS
j		1	HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD
		1	RLRDTVKALTREOEKLLGOLKEVOADKEOSEAELQVAQQENHHL
}	}	1	NLDLKEAKSWOEEOSAOAORLKDKVAOMKDTLGOAOORVAELEP
ĺ		[LKEOLRGAGELAASSOOKATLLGEELASAAAARDRTIAELHRSR
		}	LEVAEVNGKLAELGLHLKEEKCOWSKERAGLLQSVEAEKDKILK
		1	LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREL
	i		
1	`	Ì	TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
	Į.	1	EDATTEDEEAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
			ASLLLGLE
7091	186	1076	EGMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP
			EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIEAY
1	İ	1	ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD
1	1	}	SIEYGLGYDCPATEGIFDYAAA1GGATITAAQCLIDGMCKVAIN
ł	l	1	WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH
ı	i		HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY
		ļ	YSVNVPIQDGIQDEKYYQICERYEPPAPNPGL
7092	522	809	KQGINEDQEESQXPRLGEGCEPISKRQMKKLIKQKQWEEQRELR
1	}	1	KOKRKEKRKRKKLERQCOMEPNSDGHDRKRVRRDVVHSTLRLII
-		ļ	DCSFDXLM
7093	454	655	NFGVSGVELAQQASMVRMSFVIAACQLVLGLLMTSLTESSIQNS
]	1	ECPOLCVCEIRPWFTPOSTYREA
7094	2	508	FVRSMHWGVGFASSRPCVVDLSWNQSISFFGWWAGSEEPFSFYG
,	i -		DIIAFPLQDYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE
ľ	1	1	LLVIRKQQEIDSKDAIILHQFARPNNGVPSLSPFCLKMETYLRM
	Į.	1	•
	 	 	ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGTEFI1
7095	1	411	IASSLPKMASLLCSDRVIJYLVQGEKKVRAPLSQLYFCRYCSELR
1		1	SLECVSHEVDSHYCPSCLENMPSAEAKLKKNRCANCFDCPGCMH
1]]	TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD
	L	t	KSVGE
7096	224	2067	ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRPLLQELLLNNFC
1		1	SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR
}	l		APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE
			QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS
	}		EDSDSASEEDLOTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF
1	1	1	LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA
}	}	1	
(GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN
]	Į	LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF
,		1	FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE
1		[EDPREAVRLHSPOTHWKTVREERKKPTEEEIRKICRDEKEALGO
			I WEDGOVOGGGOODGOODGI TI LIET WIGHT DI CECEUI DUDED
		1	NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR
			RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL
			RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL
			rkrnkkeksrdoeagahrtilootoeeepstossgavaaplgpl ldeakapgopelwaallaacragdvgvlklolapspadprvlsl
7097	256	1228	RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL

	- 		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cystcine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
)	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, C=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	seanence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSIPGSHDTMTYC
	•		LNKKSPISHEESRLLQLLNKALPCITRPVVLKWSVTQALDVTEQ
}		}	LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDTLTEISE
		Ì	WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGDMLCPRG
}	}	}	EVPTLRQLWSRGQQVIVSYEDESSLRRHHELWPGVPYWWGNRVK
1			TEALIRYLETMKSCGR
7098	82	956	SSFLKRCRKVLGCWGIPSECSLFSTLEEPRDKEIDNYCVMRLQT
1	İ	1	EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHFHPSLEA
ļ	4	1	LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLPSKPLLG
l	!	1	LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFLGLWLVL
 	ļ	<u> </u>	LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAEGRTRGR
1	1	1	AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPVGCGCFF
1		į.	LGLALRLVYYHWLHFSCCWKPDPDOVD
7099	992	210	
, , , , ,	332	1 210	LFRLAPGFLRSLARQGYHQIWAFFFLPSGATATWPAASRSRSLA
I	1	1	ARSLPRSPARPGPNDALLGEHDFRGQGVRAQRFRFSEEPGPGAD
ł	ŀ		GAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELPHCLEVC
I	}	}	ROSCOMNNLPHLOVVGLTWGHISWDLLALPPODIILASDVFFEP
		•	EDFEDILATIYFLMHKNPKVQLWSTYQVRSADWSLEALLYKWDM
		<u> </u>	KCVHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKDSL
7100	205	671	ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPPHLSVL
]	1]	FLFSFPPQLGDFLEAFPVFKKYDRNGLNVSIECKRVSGLEPATV
			DWAFDLTKINMOTMYEOSEWGWKDREKREEMTDDRAWYLIAWEN
			SSVPVAFSHFRFDVERGDEVLYW
7101	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
1	}		VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEIT1PADVTP
			ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
		}	VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
7102	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
1	1	1	VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEIT1PADVTP
		1	ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
			VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
7103	119	438	GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEKSSSSES
)	1.	LSDKGSELKKSFDAVVFDVLKVTPEEYAGQITLMDVPVFKAIQP
		L	DELSSCGWNKKEKYSSAP
7104	1676	795	RLWEHRSVSAGASGWGLSSPGCLLLHPSLPEEERVDILINNAGV
l			MRCPHWTTEDGFEMQFGVNHLGEAWAGAAPWVQAILPRRPPKVL
1	\	[GF*V*VKSDLF1;LNPGHFLLTNLLLDKLKASAPSR1INLSSLA
1			HVAGHIDFDDLNWQTRKYNTKAAYCQS\KLAIVLFTKELSRRLQ
}		}	GSGVTVNALHPGVARTELGRHTGIHGSTFLOHHN\WAHLLAAWS
ļ		l	KSPRSWPAPAQHNTLAVAEELA\VISGKYFDGLKQKAPAPEAED
ļ		į	EEVARRLWAESARLVGLEAPSVREQPLPR
7105	765	143	GOMCRRPSPKSTSCLSMTCDLP/RGLQDPQCLALFRVAVDKHQA
1			LLKAAMSGOGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWQLST
[1	[SOIPVOOMHLEDVHNYPDYVSSGGGFGPADDHGYGVSYIFMGDG
[[Į.	MITFHISSKKSSTKTDSHRLGQHIEDALLDVASLFQAGQHFKRR
(1	1	FRGSGKENSRHRCGFLSROTGASKASMTSTDF
7106	14	1064	GLOAGHPHPRSASRIPEADTH\YSKLORAFDSIVNKDHKRMFGT
		1307	1
			YFRVGFFGSKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQCF
]	l		GAEFVEVIKDSTPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV
1		1	TYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTTMHAF
]		PYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINOEPPD
}		İ	AKMLQMVLQGSVGATVNQGPLEVAQVFLAEIPADPKLYRHHNKL
}	1	}	RLCFKEFIMRCGEAVEKNKRLITADQREYQQELKKNYNKLKENL
1			
7107	1145	591	RPMIERKIPELYKPIFRVESOKRDSFHRSSFRKCETQLSQGS *1*WLQTGKKK

SEQ	Fredicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotid-	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, J=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	F=Proline, O=Glutamine, R=Arginine,
}	zmino acid residue of	amino acic	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Sequence	\=possible nucleotide insertion)
7108	1	942	VKVALLTNLEQPRIESEWENSPILKMFLFQFVNLNSSIFYIAF
/100	1	3.32	FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMOMGIIWVLK
}			OTWNNFMELGYPLIONWWTRRKVRQEHGPERKISFPQWEKDYNL
1		1	CPMNAYGLFDEYLEMILOFGFTTIFVAAFPLAPLLALLNNIIEI
			RLDAYKFVTOWRRPLASRAKDIGIWYGILEGIGILSVITNAFVI
Ì			Altsdfiprlvyaykygpcagogeagokcmvgyvnaslsvfris
			DFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF
Į.			WEVLAW
7109	964	102	WDORKENSLVPGPAHGPAGEEPWEKKESLGAAGEALS1QLQPKE
		1	TOPFPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF
	ļ		SEKLATOTSTFEATSEGTLELQQRNPKAERLRWSPAQEESFRQM
	}		VVIHKEIPTGKKDHECSECGKTFIYNSHLVVHQRVHSGEKPYKC
	1	1	SDCGKTFKQSSNLGQHQRIHTGEKPFECNECGKAFRWGAHLVQH
1)	1	CRIHSGEKPYECNECGKAFSQSSYLSQHRRIHSGEKPF1CKECG
	<u> </u>		KAYGWCSELIRHRRVHARKEPSH
7110	96	697	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKOMLTRASITPVLG
ļ			SPSTKRRGQMLQPI1EGETAHFFEEIKEEEEDGVNLSSELGDML
{	l l		KTAVQVQSSLKNSESDVEENQEKLALDLRLSSSRAASMPELLEQ
	İ		LWKARAEKKKLRKTLREFEEAFYQQNGRNAQKEDRVPVLEEYRE YKKIKAKLRLLEVLISKODSSKSI
7111	2	414	GSGLYRGFTPGGOCIWKPNSMPPDHERNFGFTQFALELNELTAE
/ + + 1	2	313	LKRSLPSTDTRLRPDQRYLEEGNIQAAEAQKRRIEQLORDRKKV
ì	j		MEENNI VHOARFFRROTDSSGKEWWVTNNTYWRLRAEPGYGNMD
			GAVLW
7112	103	495	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW
ļ	ļ		FKNDQDIQLSEHFSVKVEQAKYVSMTIKGVTSEDSGKYSINIKN
	1		KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
7113	1	824	KCLRQAWHEAPSSLAFTRWCSREERAEGGGNLHRSITRDPKPPG
1		j	LEPSQRPMDDKKKKRSPKPCLAQPAQAPGTLRRVPVPTSHSGSL
}		1	ALGLPHLPSFKQRAKFKRVGKEKCRPVLAGGGSGSAGTPLQHSF
	ì .		1.TEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEQLEHVREM
1	1		OEKLARLHFSLDVCGEEEDDEEEEDGVTEGLPEEQKKTMADRNL
	1		DOLLSNIESCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK SSGPLNLPRR
7114	3	1492	VWEVDEQIDHYKESODKFLWQAAFIGKETLKDESGQECKICRKI
1114	1 3	1436	IYLNTDFVSVKQRLPKYYSWERCSKHHLNFLGONRSYVRKKDDG
			CKAYWKVCLHYNLHKAOPAERFFDPNQRGKALHQKQALRKSQRS
	1		QTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF
			SOKSTLIAHORTHTGEKPYECSECGKTFIQKSTLIKHQRTHTGE
	Ì		KPFVCDKCPKAFKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ
1.	1		RIHTSEKPOCSEHGKASDEKPSPTKHWRTHTKENIYECSKCGKS
	1		FREKSHLSVHQRIHTGEKPYECSICGKTFSGKSHLSVHHRTHTG
	l		EKPYECRRCGKAFGEKSTLIVHQRMHTGEKPYKCNECGKAFSEK
			SPLIKHQRIHTGERPYECTDCKKAFSRKSTLIKHQRIHTGEKPY
i	{		KCSECGKAFSVKSTLIVHHRTHTGEKPYECRDCGKAFSGKSTLI
		<u> </u>	KHORSHTGDKNL
7115	1	947	NAAHGYNWGLWCMYIIPPQDWLDRGDESAPIRTPAMIGCSFVVD
ì	1		REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA
	1	1	HIERTRKPYNNDIDYYAKRNALRAAEVWMDDFKSHVYMAWNIPM
j	1		SNPGVDFGDVSERLALRQRLKCRSFKWYLENVYPEMRVYNNTLT
	l		YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSADGL
	1		LOLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTORLWD
	[PTOSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN
7336		 	WI KHARH
7116	866	95	RVRMRRNAEVIEEKLSMKSWAKFRPGEPWKGYPNIDPETDFYVT
!	l .	1	PGSVINNLSINTVREVDHLRDRNSGSSSSLNTTLPSTSAWSSIR

Deginning nucleotide coation coation coation coation coation coation coation coation coation coation coation corresponding to first amino acid amino acid sequence sequence coation co	SEO	Predicted	Predicted end	Amino acid segment containing signal peptice
Note	1 -	I .		
corresponding		1 -	1	
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence sequence (amino acid sequence sequence (amino acid sequence	1		I .	
to first amino acid residue of amino acid amino acid residue of amino acid sequence sequence #TYPTOPIAN, Y-TYPTOPIAN, Y-UNIANE, #TYPTOPIAN, Y-TYPTOPIAN, Y-STOP Codon, /-possible nucleotide deletion, V-possible nucleotide insertion) ASNYNVPLSSTAGGTSARNSDSKITWSPGSVINTSLAHELRKYP LPRKHTAPSRPPPGUTGNEPLSTWINSPURICEGMONSDARY TPOSSWOESS SCRITHWINIAUDITOOLDSSTLATLOWGHCPLJT PHARLPHONALWAYS SKEEVYAKONSHISLELLTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SKEEVYAKONSHISLELTRYP THARLPHONALWAYS SK	1			
amino acid residue of amino acid sequence Sequence Codon, /-possible nucleotide deletion, V-	ł			
residue of amino acid sequence (Codon, /-possible nucleotide deletion, V-possible nucleotide d	1			
Sequence Codom, /=possible nucleotide deletion,	1	1		
Appossible nucleotide insertion	}		E .	Codon /-nossible nucleotide deletion
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EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITOTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESOPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRROFQSLDTTMRRLIPFFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF				•
DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPX SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITOTLQDLLKALKGLVVWSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APPELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPPHNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRROFQSLDTTMRRLIPFFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	1			
LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITOTLQDLLKALKGLVVMSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APPELTQRPQVGCYIHGLPLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRROFQSLDTTMRRLIPFFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF				-
SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESOPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRROFQSLDTTMRRLIPFFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	}			
MNTVLVQEVIRYNRLLQVITOTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESOPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRFWVLSLGSMVGLMTTGRROFQSLDTTMRRLIPFFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF				
ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESOPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 S46 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPFFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	1			
IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDT:SFDFKVMFE APSELTQRPQVGCYIHGLPLEGARWDPEAFQLAESOPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPFFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	1			le de la companya de la companya de la companya de la companya de la companya de la companya de la companya de
APSELTQRPQVGCYIHGLPLEGARWDPEAFQLAESOPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPFFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF				
AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPFFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF)			
AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPFFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF				APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM
7121 2 546 RPLRPWVLSLGSMVGLMTYGRROFQSLDTTMRRL1PFFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALOEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF				AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI
LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF				AVEIPTHQPQRHWIKRGVALICALDY
SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	7121	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRL1PFFREASAK
				LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV
GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL				SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF
				GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
140:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=beucine, M=Methionine, N=Asparagine,
1	to first.	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid		1
1		residue of amino acid	S=Serine, T=Threonine, V=Valine,
1	residue of		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	eequenc€		\=possible nucleotide insertion;
			ETRQE
7122	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK
1	1		LTTLVDADAEAFTAYLEAMRLFKNTPEEKDRRTAALQEGLRRAV
			SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF
1			GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL
L			ETRQE
7123	1	1092	KPAVPEARSAGTSEAGRSGAEEVSCGSVSGDGAAMRLTPRALCS
1	1		AAQAAWRENFPLCGRDVARWFFGHMAKGLKKMQSSLKLVDCIIE
}	}	,	VHDARIPLSGRNPLFQETLGLKPHLLVLNKMDLADLTEQQKIMQ
		,	HLEGEGLKNVIFTNCVKDENVKQIIPMVTELIGRSHRYHRKENL
1	1		EYCIMVIGVPNVGKSSLINSLRRQHLRKGKATRVGGEPGITRAV
1	}	ļ	MSKIQVSERPLMFLLDTPGVLAPRIESVETGLKLALCGTVLDHL
1			VGEETMADYLLYTLNKHQRFGYVQHYGLGSACDNVERVLKSVAV
]	KLGKTQKVKVLTGTGNVNVIQPNYPAAARDFLQTFRRGLLGSVM
1	1		LDLDVLRGEPRV
7124	2	382	LPLTLLLAAPFAHLLLPPGHDOSPCWHPGPALSPGTLGPLSWAM
•	1		ANSGLQLLGYFLALGGWVGIIASTALPQWKQSSYAGDASIQLRS
1		1	KVFVLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
7125	166	1127	NCISEKRNYSFSMQKGKGRTSR1RRRKLCGSSESRGVNESHKSE
			FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLQEGQMIIS
l .		Į.	LPESCLLT\RDTVIRSYLGAY1TKWKPPPSFLLALCTFLVSEKH
1			AGHRSLLEA\YLEILPKAYTCPVCLEPEVVNLLPKSLKAKAEEQ
1 .			RAHVQEFFASSRDFFSSLQPLFAEAVDSIFSYSALLWAWCTVNT
			RAVYL\SPGSGNAFLQSRTPVCLAPYLDLLNHSPHVQVKAAFNE
	1		ETHSYEIRTTSRWRKHEEVFICYGPHDNQRLFLEYGFVSVHNPH
1		Ì	ACVYVSRGWNQLCS
7126	1	733	CRDMAAFIVPSPARRCSOKGSLGHLPTOPWLWAAMSPRGQERGT
1			SHSQAREPORPGRWLLGSLQSSPGTLGQAGTASRRRGCMVQRWV
1			QVATGRRAVQVPKGALGLALGETSPGASRGMSGGAGGCWALGWA
1			PSPVLPSWLLEGPPPWLSIISDSGTQRPSPRRCPARPSPWGPQC
ł			WRGGRIASAEASST*TPGSGSRARSGRRSPGSRRRSASAPSPTP
1			PTDACA*SCVARPAGSRSSRPAAA
7127	1311	277	GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKEI*RRIPRIF
1		[AKQKQI+S+NSQKIGASEIDRGRKEADCSDAPAAARIGAVSVFR
1			RSTOEARVSPRSNAKSANLRAVRAD*WEHFVLLFHTPEQFLAEC
1	1	,	ICRST**K*WHOLC*PLSSL*TGLKRKLLL*VLFRI*WLKDCDV
1			*FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*HIMNLLLPM*L
İ]	COSSLRDQTIVTWRM*RNYSMFRINMISSL*DGSIHIPLKLHFY
1			PALIFTLTVPINSCCORPLPLFAHQSIKTLASSGSPMLACLRFL
1	i		LVKKRAFIHTPRSPGCSV*CKHVLVKDNKNNCVGSEV
7128	2	5228	GRVDLWTILLGRSALRELSOIEAELNKHWRRLLEGLSYYKPPSP
	1	3220	SSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCYLQE
1	1		DYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHL
	1		LTYFQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTRAPT
}]	}	WETHGNLMTEROVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSD
1	i		LLVLTKMFKEOGFGSRQTNRHLVDETMDPFVDRIGYFSALILVE
]	1		GMDIESLHKCALDDRRELHQFAODGLICQDMDCLMLTFGDIPHH
1	}		
1		İ	APVLLAWALLRHTLNPEETSSVVRKIGGTAIOLNVFOYLTRLLQ
1	1		SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDTA
}	1		CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLL
	1		RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWR
1	1		ROTPKLLYPLGGCTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSW
ı	1		TLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIA
1	1		DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNCLTVLAARNPA
1	1	}	kvwtdlrhtgflpfvahpvsslsomisaegmnaggygnllmnse
1]	QPQGEYGVTIAFLRLITTLVKGQLGSTQSQGLVPCVMFVLKEML

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
	1	ł	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
í	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
\	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	
ì			S=Serine, T=Threonine, V=Valine,
· f	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
	 	 	PSYHKWRYNSHGVREOIGCLILELIHAILNLCHETDLHSSHTPS
1			LOFLCICSLAYTEAGOTVINIMGIGVDTIDMVMAAOPRSDGAEG
1	ł		
1			QGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGAH
	1		GNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLG
1		1	NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\VETQP
1		!	GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV/VWELIDSQQ
ŀ	1		QDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKFWENLT
Į		}	, -
1	1	Ĭ	SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQP
ļ	ļ		LKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYQM
1		1	LVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV
1			PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEG
I			VLOADOOLMEKTKAKVFSAFITVLOMKEMKVSDIPOYSOLVLNV
1		Į.	CETLOEEVIALFDOTRHSLALGSATEDKDSMETDDCSRSRHRDQ
1	,	1	-
I			RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEV
			SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSICLPL
			LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQLLKT
1	1	·	LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADHTVG
	ì	ļ	FILOLSNFMKEWHFHLPOLMRDIOVNLGYLCOACTSFLHSRKML
1	i	1	OHYLONKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAADTE
1	1	1	
1	1		ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLA
i	ŀ		EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELDKKK
	l .		EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRYLRD
	1		PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATGVLP
-	1		SPOGKSTSLSKASPESQEPLIQLVQAFVRHMQR
7129	 	1054	FRRFRWRRLH*AGPASSAGGSPGEASGTMSGELPPNINIKEPR
1 122	1 *	1054	WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQGIV
	1	Į.	1 -
i .			PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNMTI
1	ļ		TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVNEL
ı	f	1	GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAANCI
	Į		NIPLMRORELKVGIPVTDENGNRLGESANAAKQAITQVVVSRIL
1	1		MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIOVGLVGFCLVFA
į.		ł	TPLCCALFPOKSSMSVTSLEAELQAKIQESHPELRRVYFNKGL
	ļ		
7130	2	760	HEVPSLOTSDPLPGSVQRCSVVVSQPNXENWCODHLYNSLGRKG
[1	ISAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLHRSS
1		1	RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLPLN
1	i		AQIATQNYFSNFKETDGDEDDYVEIKSEEDESELELSHNRRRKS
1	ļ	1	DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYLTP
1	İ	ļ	YNDSDKLNDYLWRGPSPNQONIVOSLREKFQCLSSSSFA
77.33	005	F20	
7131	805	573	AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLUDAVQFNHLEVV
L	1	1	KLLQDYQDSYTLSETQAEAAAEALSKENLESMV
7132	1420	1067	IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTVTA
1		}	IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLFLI
	1		RLIHKELSCPGSATGDOVPFKEO
7133	+	1-3640	QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLEKF
1 /133	2	3648	
ł	1		EEELLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGFVQ
1	Į.		RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRSRL
1			RLPEMVGHPAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLACMH
	1		MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSASMS
1 '	I	}	SEEVKQVESGTLRFOFSLGSEEHLDAPTEPVSGPKVERRPSRKP
			1 2FF AVÃAF9GIRKIĞI 9TG9FFUDNAKI FRA9GEKAFKKAŞKKA
ı		i	PROPOSED
			PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQHCL
			PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQHCL ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS
			· · · · · · · · · · · · · · · · · · ·
			ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP
			ARPTSOLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS
			ARPTSOLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS RVAQDCRGTSWPKTVYFTFQFYRFPPATTPRLQLVQLDEAGQPS
			ARPTSOLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS

	T Book at a King and a second	T Salar are a series	<u></u>
SEC	Predicted	Predicted end	Amino acid Eegment containing signal peptide
ID NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NU:	location	-	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		ì	LEVVATEYEQDNMVVSGDMLGFGRVKPIGVHSVVKGRLHLTLAN
			VGHPCEQKVRGCSTLPPSRSRVISNDGASRFSGGSLLTTGSSRR
	i		KHVVQAQKLADVDSELAAMLLTHARQGKGPQDVSRESDATRRRK
			LERMRSVRLOEAGGDLGRRGTSVLAQQSVRTQHLRDLQVIAAYR
		ļ	ERTKAESIASLLSLAITTEHTLHATLGVAEFFEFVLKNPHNTQH
		j	TVTVEIDNPELSVIVDSQEWRDFKGAAGLHTPVEEDMFHLRGSL
]	APQLYLRPHETAHVPFKFQSFSAGQLAMVQASPGLSNEKGMDAV
			SPWKSSAVPTKHAKVLFRASGGKPIAVLCLTVELQPHVVDQVFR
		j	FYHPELSFLKKAIRLPPWHTFPGAPVGMLGEDPPVHVRCSDPNV
	1	}	ICETQNVGPGEPRDIFLKVASGPSPEIKDFFVIIYSDRWLATPT
			QTWQVYLHSLQRVDVSCVAGQLTRLSLVLRGTQTVRKVRAFTSH
		1	PQELKTDPKGVFVLPPRGVQDLHVGVRPLRAGSRFVHLNLVDVD
			CHQLVASWLVCLCCRQPLISKAFEIMLAAGEGKGVNKRITYTNP
		Į	YPSRRTFHLHSDHPELLRFREDSFQVGGGETYTIGLQFAPSORV
	<u> </u>	1	GEEEILIYINDHEDKNEEAFCVKVIYQ
7134	2115	1111	GGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEEGLIDNSG
)	LRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTL
		1	ECLEEALEAEKPSGIHVFAVLLHAHLAGRGIRLRHFRKGKEMKL
		}	LAYDDDFDFNFQEFQYLKEEQTILPGDNLITECRYNTKDRAEMT
		1	WGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEI
		\	YRPVTTWPFIIKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVL
		1	SLPVNVRCSKTDNAEWSIQGMTALPPDIERPYKAEPLVCGTSSS
			SSLHRDFSINLLVCLLLLSCTLSTKSL
7135	2	2072	FVPRVTPRSLSLOGPKGESVGSITQPLPSSYLIFRAASESDGRC
			WLDALELALRCSSLLRLGTCXPGRDGEPGTSPDASPSSLCGLPA
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR
		1	KTESGSDOSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE
		Į.	ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH
		Į.	ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG
	1		ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS
		1	GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG
	1	1	ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI
		}	SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR
		f	QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL
	:	1	EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP
			LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL
	}		RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC
	1	1	PRCRKEARRLQALEEAILSIREAQQELHRHLSAMLSSTARAAQA
	<u> </u>		PTPGLLQSPRSWFLLCVFLACQLFINHILK
7136	2	418	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK
	!	1	SQQRKVRQMIEQLONSKAV1QSKDATIQELKEKIAYLEAENLEM
	:	1.	HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV
	<u></u>	<u> </u>	IRVVET
7137	2	46€	WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA
		1	GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI
	1	i	PDDLDGNTNKRSKEVRVLQEMOLLQVAAMNYRLRPLEKFVTYFT
		1	RMEQLSDKESYKLSCQLEPENP
7138	2	466	WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA
		1	GSFKVATQERNPORAQMRLRRQKKGVVPFLGDFLTELQRLDSAI
			PDDLDGNTNKRSKEVRVLOEMOLLQVAAMNYRLRPLEKFVTYFT
			RMEQLSDKESYKLSCQLEPENP
	4	 	
7139	1	45/	
7139	1	357	SLRNSARGLKMAASAARGAAALRRSINOPVAFVRRIPWTAASSQ LKEHFAOFGHVRRCILPFDKETGFHRGLGWVOFSSEEGLRNALO
7139	1	35/	LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ
			LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF
7139	1401	1957	LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
!	corresponding .	to first	L=Leucine, M=Methichine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
 	sequence		•
			QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ
1			WTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF
			ADFMTNQCG
7141	124	1073	LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL
	i '		VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD
1	'		EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP
ĺ			VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK
			EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA
			AASEETRAAKLRGAAAKSSCOLPIPSAIPRPASRMPLTSRSVPP
1			GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM
L			GATRSNLQPP
7142	658	839	LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL
1			KK*SRAVGVVVVMCRT/YSSDLQVGVİKPWLLLGSQDAAHDLDT
			LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP
}			ECFEFIEEAKRKDGVVLVHCNA
7143	3	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ
1	ĺ		GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG
1			VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA
ł			SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR
			KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG
1	į		HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI
7144	1	988	FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR
1			RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD
			SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS
l			DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR
			QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII
1			VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLNRDGTQCLS
			GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG
			RDRKIYCTDLRNPDIRVLICE

TRADOCS:1416260.1(%CSK01!.DOC)

WHAT IS CLAIMED IS:

- 1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.
- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.
- ·13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex;
 and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).

- 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.
- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

International application No.

PCT/US00/34263

A. CLA. IPC(7)	SSIFICATION OF SUBJECT MATTER : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/8	2 15/9 5: COTK 14/00	
US CL	: 536/23.1; 435/320.1, 455, 468, 530/300, 350		
	International Patent Classification (IPC) or to both na	etional classification and IPC	
B. FIEL	DS SEARCHED		
	cumentation searched (classification system followed 36/23.1; 435/320.1, 455, 468, 530/300, 350	by classification symbols)	
Documentati	on searched other than minimum documentation to the	extent that such documents are included i	n the fields searched
Electronic da MEDLINE,	ata base consulted during the international scarch (nam EAST	or of data base and, where practicable, sea	rch terms used)
C. DOC	UMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where a	ppropriate, of the relevant passages	Relevant to claim No.
Α .	WAJIMA et al. The cDNA cloning and transient ex hydroxysteroid dehydrogenase of chickens. Gene. 1	pression of an ovary-specific 17beta-	1-11, 13-16, and 19-26
A	US 5,175,095 A (MARTINEAU et al) 29 Decembe columns 3-18.	r 1992 (29.12.1992), see especially	1-11, 13-16, and 19-26
Α	Database PubMed, ID No. 2393392, FREUDENST inhibitor of metalloproteinase: sequence and express Biophys. Res. Commun. August 1990. Vol.171. No.	ion in bovine ovarian tissue. Biochem.	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract		1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2760883, BEIL et al. Sy the baboon (Papio anubis). J. Reprod. Fertil. July 19 Abstract.	onthesis of polypeptides by the cervix of 1989. Vol.86. No.2. pages 535-544, see	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6, pages 2050-2053, see Abstract.		1-11, 13-16, and 19-26
Further	documents are listed in the continuation of Box C.	See patent family annex.	
• 5	pecial calegories of cited documents:	"T" later document published after the inte	
	defining the general state of the art which is not considered to be lar relevance	date and not in conflict with the applic principle or theory underlying the inve	ntion
	plication or patent published on or after the international fitting date	"X" document of particular retevance; the considered novel or cannot be consider when the document is taken atome	
	which may throw doubts on priority claim(s) or which is cited to the publication date of another citation or other special reason (as	document of particular relevance; the considered to involve an inventive step	when the document is
	referring to an oral disclosure, use, exhibition or other means	combined with one or more other such being obvious 'D a person skilled in the	
priority d	published prior to the international filing date but later than the ate claimed	document member of the same patent f	
Date of the actual completion of the international search Date of mailing of the international search report 7 100 2001			ch report
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT		Authorized officer Sir Marsh Michael Woodward	Allen In
Wasi Facsimile No	hington, D.C. 20231 . (703)305-3230	Telephone No. (703)/308-0196	

international application No.

PCT/US00/34263

Box 1 Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box 11 Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows: This includes 4 invention Groups and 3572 sequence species
 As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

International application No.

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This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group 1, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group IV, claim 17-18, drawn to method of indentifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

Form PCT/ISA/210 (extra sheet) (July 1998)

CORRECTED VERSION

(19) World Intellectual Property Organization International Bureau



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	09/598,042	9 July 2000 (09.07.2000)	US
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29 November 2000 (29.11.2000)

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[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.



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US	09/620.312 (CIP)
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US	09/653,450 (C1P)
Filed on	3 August 2000 (03.08.2000)
US	09/662.191 (CIP)
Filed on	14 September 2000 (14.09.2000)
US	09/693.036 (CIP)
Filed on	19 October 2000 (19.10.2000)
US	09/727,344 (CIP)
Filed on	29 November 2000 (29.11.2000)

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[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

01/5331



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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

REVISED VERSION

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/34263

A. CLASSIFICATION OF SUBJECT MATTER 1PC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00								
US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350 According to International Patent Classification (IPC) or to both national classification and IPC								
B. FIELDS SEARCHED								
Minimum documentation searched (classification system followed by classification symbols) U.S.: 536/23.1; 435/320.1, 455, 468, 530/300, 350								
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched								
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) MEDLINE, EAST								
	JMENTS CONSIDERED TO BE RELEVANT							
Category *	Citation of document, with indication, where ap		Relevant to claim No.					
^	WAJIMA et al. The cDNA cloning and transient exp hydroxysteroid dehydrogenase of chickens. Gene. 19	1-11, 13-16, and 19-26						
A	US 5,175,095 A (MARTINEAU et al) 29 December columns 3-18.	1-11, 13-16. and 19-26						
A	Database PubMed, ID No. 2393392, FREUDENSTE inhibitor of metalloproteinase: sequence and expressi Biophys. Res. Commun. August 1990. Vol.171. No.	1-11, 13-16, and 19-26						
A,P	Database PubMed, ID No. 10919256, HENNEBOL generation and characterization of an ovary-selective library. Endocrinology. August 2000. Vol.141. No.8	1-11, 13-16, and 19-26						
A	Database PubMed, ID No. 2760883, BEIL et al. Synthe baboon (Papio anubis). J. Reprod. Fertil. July 19 Abstract.	1-11, 13-16, and 19-26						
A,P	Database PubMed, ID No. 10830289. HINSHELWC upstream of the human CYP19 (aromatase) gene med transgenic mice. Endocrinology. June 2000. Vol.141	1-11, 13-16, and 19-26						
Further	documents are listed in the continuation of Box C	See patent family annex.						
• s	pecial categories of cited documents:	"T" later document published after the inte date and not in conflict with the applie						
"A" document defining the general state of the art which is not considered to to of particular relevance.		principle or theory underlying the inv	ention					
"E" earlier application or patent published on or after the international filing ear		considered novel or cannot be considered when the document is taken alone						
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another cutation or other special reason (as specified)		"Y" document of particular relevance; the claimed invention cannot be considered to invoive an inventive step when the document is combined with one or more other such documents, such combination						
"O" documen	it referring to an oral disclosure, use, exhibition or other means	being obvious to a person skilled in th	ne art					
	a published prior to the international filing date but later than the date claimed	"&" document member of the same patent family						
Date of the actual completion of the international search Date of mailing of the international search report								
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Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REF PCT/US00/34263 Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet) This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons: Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely: Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically: Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a). Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet) This International Searching Authority found multiple inventions in this international application, as follows: This includes 4 invention Groups and 3572 sequence species As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos...

No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-11, 13-16, and 14-26

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

Remark on Protest

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group 1, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group IV, claim 17-18, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

Form PCT/ISA/210 (extra sheet) (July 1998)

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